93410

STIC-Biotech/ChemLib

From: Schultz, James
Sent: Wednesday, May 07, 2003 9:22 AM
To: STIC-Biotech/ChemLib
Subject: Sequence search 10/057,550

Whoops, sorry, the corrected file name is now listed in the title above.

-----Original Message-----
From: STIC-Biotech/ChemLib
Sent: Wednesday, May 07, 2003 9:06 AM
To: Schultz, James
Subject: RE: Sequence search pct/us02/04123

This Application Number does not have a valid CRF - please provide the necessary correction or another application number.
maude

-----Original Message-----
From: Schultz, James
Sent: Wednesday, May 07, 2003 8:36 AM
To: STIC-Biotech/ChemLib
Subject: Sequence search pct/us02/04123

Hello,
I need a length limited nucleotide sequence search performed on SEQ ID NO: 64 in the above entitled application, where the maximum size of the returned hit is no more than 50 nucleotides long. Thanks,
Doug Schultz

J. Douglas Schultz, Ph.D.
AU 1635 (Biotechnology)
Patent Examiner
United States Patent and Trademark Office
(703) 308-9355
(703) 746-3973 (fax)
Office: CM1 12E18
Mail: CM1 11E12

Edward Hart
Technical Info. Specialist
STIC/Biotech
CMI 6B02 Tel: 305-9203

Searcher:_____
Phone:_____
Location:_____
Date Picked Up: 5/8/03
Date Completed: 5/7/2003
Searcher Prep/Review:_____
Clerical:_____
Online time:_____

TYPE OF SEARCH:
NA Sequences: 1
AA Sequences:_____
Structures:_____
Bibliographic:_____
Litigation:_____
Full text:_____
Patent Family:_____
Other:_____

VENDOR/COST (where applic.)
STN:_____
DIALOG:_____
Questel/Orbit:_____
DRLink:_____
Lexis/Nexis: XXX
Sequence Sys.: 101
WWW/Internet:_____
Other (specify):_____

STIC SEARCH RESULTS

Biotech-Chem Library

Questions about the scope or the results of the search? Contact ***the searcher or contact:***

Mary Hale, Information Branch Supervisor
308-4258, CM1-1E01

Voluntary Results Feedback Form

- *I am an examiner in Workgroup:* ☐ *Example: 1610*
- *Relevant prior art **found**, search results used as follows:*
  - ☐ 102 rejection
  - ☐ 103 rejection
  - ☐ Cited as being of interest.
  - ☐ Helped examiner better understand the invention.
  - ☐ Helped examiner better understand the state of the art in their technology.

Types of relevant prior art found:

- ☐ Foreign Patent(s)
- ☐ Non-Patent Literature
  (journal articles, conference proceedings, new product announcements etc.)

- *Relevant prior art **not found:***
  - ☐ Results verified the lack of relevant prior art (helped determine patentability).
  - ☐ Results were not useful in determining patentability or understanding the invention.

Comments:

Drop off or send completed forms to STIC/Biotech-Chem Library CM1 – Circ. Desk

GenCore version 5.1.4_p5_4578

OM nucleic - nucleic search, using sw model

Run on: May 16, 2003, 05:03:09 ; Search time 7722 Seconds
(without alignments)
11219.769 Million cell updates/sec

Title: US-10-057-550A-64
Perfect score: 2977
Sequence: 1 ccgaatgtgaccgcctcccg.....taataaaataaattaaattt 2977

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 2054640 seqs, 14551402878 residues

Total number of hits satisfying chosen parameters: 841850

Minimum DB seq length: 0
Maximum DB seq length: 50

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: gb_ba:*
2: gb_htg:*
3: gb_in:*
4: gb_om:*
5: gb_ov:*
6: gb_pat:*
7: gb_ph:*
8: gb_pl:*
9: gb_pr:*
10: gb_ro:*
11: gb_sts:*
12: gb_sy:*
13: gb_un:*
14: gb_vi:*
15: em_ba:*
16: em_fun:*
17: em_hum:*
18: em_in:*
19: em_mu:*
20: em_om:*
21: em_or:*
22: em_ov:*
23: em_pat:*
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25: em_pl:*
26: em_ro:*
27: em_sts:*
28: em_un:*
29: em_vi:*
30: em_htg_hum:*
31: em_htg_inv:*
32: em_htg_other:*
33: em_htg_mus:*
34: em_htg_pln:*
35: em_htg_rod:*
36: em_htg_mam:*
37: em_htg_vrt:*
38: em_sy:*
39: em_htgo_hum:*
40: em_htgo_mus:*
41: em_htgo_other:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.		Score	% Query Match	Length	DB	ID	Description
1		32.8	1.1	49	9	HUMRAF12	L00213 Human c-raf
2		30.6	1.0	31	6	AX248756	AX248756 Sequence
3		28	0.9	28	6	AR090859	AR090859 Sequence
4		28	0.9	28	6	AR197894	AR197894 Sequence
c 5		26	0.9	26	6	AR090860	AR090860 Sequence
c 6		26	0.9	26	6	AR197895	AR197895 Sequence
c 7		26	0.9	26	6	I96168	I96168 Sequence 5
8		26	0.9	26	6	I96169	I96169 Sequence 6
c 9		25	0.8	25	6	AR110776	AR110776 Sequence
c 10		22.2	0.7	50	6	AX157157	AX157157 Sequence
11		22	0.7	43	6	AR079693	AR079693 Sequence
12		22	0.7	43	6	AR081223	AR081223 Sequence
13		22	0.7	43	6	AR142002	AR142002 Sequence
14		22	0.7	43	6	AR170583	AR170583 Sequence
c 15		22	0.7	50	6	AX164948	AX164948 Sequence
c 16		21.6	0.7	50	6	AX159540	AX159540 Sequence
17		21.4	0.7	40	6	AR100922	AR100922 Sequence
18		21.4	0.7	40	6	AR100937	AR100937 Sequence
19		21.2	0.7	35	6	A63574	A63574 Sequence 15
20		21.2	0.7	44	9	HUMMACG	L37694 Homo sapien
c 21		21	0.7	31	6	AX119347	AX119347 Sequence
c 22		21	0.7	40	6	AR100923	AR100923 Sequence
c 23		21	0.7	40	6	AR100938	AR100938 Sequence
c 24		20.8	0.7	27	6	A63567	A63567 Sequence 8
25		20.6	0.7	21	6	AX096685	AX096685 Sequence
c 26		20.6	0.7	36	6	AX119579	AX119579 Sequence
c 27		20.6	0.7	50	6	AX159538	AX159538 Sequence
c 28		20.4	0.7	27	6	A63562	A63562 Sequence 3
c 29		20.4	0.7	27	6	A63571	A63571 Sequence 12
c 30		20.4	0.7	27	6	A63572	A63572 Sequence 13
c 31		20.4	0.7	30	6	AR208293	AR208293 Sequence
c 32		20.4	0.7	33	6	AR027238	AR027238 Sequence
c 33		20.4	0.7	40	6	AX147000	AX147000 Sequence
34		20.4	0.7	50	6	AX426994	AX426994 Sequence
35		20.2	0.7	33	6	AX253351	AX253351 Sequence
36		20.2	0.7	33	6	AX253358	AX253358 Sequence
37		20.2	0.7	38	6	AX183838	AX183838 Sequence
38		20.2	0.7	45	9	HUMNF2B	L27066 Human neuro
39		20.2	0.7	46	6	AX287576	AX287576 Sequence
40		20.2	0.7	46	6	AX287580	AX287580 Sequence
41		20.2	0.7	48	6	AX277277	AX277277 Sequence
c 42		20.2	0.7	48	6	I58003	I58003 Sequence 11
c 43		20	0.7	20	6	A52104	A52104 Sequence 7
c 44		20	0.7	20	6	A52105	A52105 Sequence 8
c 45		20	0.7	20	6	A52132	A52132 Sequence 5

ALIGNMENTS

RESULT 1
HUMRAF12
LOCUS HUMRAF12 49 bp DNA linear PRI 08-JAN-1995
DEFINITION Human c-raf-1 proto-oncogene, exon 2, clones lambda-(2,13).
ACCESSION L00213
VERSION L00213.1 GI:190830
KEYWORDS c-myc proto-oncogene; raf protein; raf proto-oncogene.
SEGMENT 2 of 9
SOURCE Homo sapiens (tissue library: of Lawn et al.) DNA.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 49)
AUTHORS Bonner,T.I., Kerby,S.B., Sutrave,P., Gunnell,M.A., Mark,G. and
Rapp,U.R.

```
  TITLE     Structure and biological activity of human homologs of the raf/mil
            oncogene
  JOURNAL   Mol. Cell. Biol. 5 (6), 1400-1407 (1985)
  MEDLINE   85295973
   PUBMED   2993863
COMMENT     See comment in segment 1.
FEATURES             Location/Qualifiers
     source          1. .49
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                     /db_xref="taxon:9606"
                     /map="3p25"
                     /tissue_lib="of Lawn et al,"
                     /tissue_lib="of Lawn et al."
     intron          <1. .15
                     /gene="RAF1"
                     /note="G00-119-546"
                     /number=1
     exon            16. .43
                     /gene="RAF1"
                     /note="G00-119-546"
                     /number=2
     intron          44. .>49
                     /gene="RAF1"
                     /note="G00-119-546"
                     /number=2
BASE COUNT       12 a      11 c      10 g      16 t
ORIGIN      About 3.7 kb after segment 1; chromosome 3p25.

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  Best Local Similarity   94.4%;  Pred. No. 1.1e+03;
  Matches   34;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy     956 TGATTGAGGATGCAATTCGAAGTCACAGCGAATCAG 991
           || || |||||||||||||||||||||||||||||||
Db       8 TGTTTCAGGATGCAATTCGAAGTCACAGCGAATCAG 43


RESULT 2
AX248756
LOCUS       AX248756                31 bp    DNA     linear   PAT 28-SEP-2001
DEFINITION  Sequence 835 from Patent WO0166800.
ACCESSION   AX248756
VERSION     AX248756.1  GI:15863379
KEYWORDS    .
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 31)
  AUTHORS   Cargill,M., Ireland,J.S. and Lander,E.S.
  TITLE     Human single nucleotide polymorphisms
  JOURNAL   Patent: WO 0166800-A 835 13-SEP-2001;
            WHITEHEAD INSTITUTE FOR BIOMEDICAL RESEARCH (US)
FEATURES             Location/Qualifiers
     source          1. .31
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
BASE COUNT        7 a       9 c       5 g       9 t       1 others
ORIGIN

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  Best Local Similarity   96.8%;  Pred. No. 4.8e+03;
  Matches   30;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy    2144 CCCTTTCTCCAGAGGCAGAACACATGTTTTC 2174
           |||||||||||||||:|||||||||||||||
Db       1 CCCTTTCTCCAGAGGYAGAACACATGTTTTC 31


RESULT 3
AR090859
LOCUS       AR090859                28 bp    DNA     linear   PAT 07-SEP-2000
DEFINITION  Sequence 979 from patent US 5994076.
ACCESSION   AR090859
VERSION     AR090859.1  GI:10017614
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 28)
  AUTHORS   Chenchik,A., Jokhadze,G. and Bibilashvilli,R.
  TITLE     Methods of assaying differential expression
  JOURNAL   Patent: US 5994076-A 979 30-NOV-1999;
FEATURES             Location/Qualifiers
     source          1. .28
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BASE COUNT        5 a       8 c       5 g      10 t
ORIGIN

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  Best Local Similarity   100.0%;  Pred. No. 2.7e+04;
  Matches   28;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy    1704 CAGTTTCCAGTCGGATGTCTACTCCTAT 1731
           ||||||||||||||||||||||||||||
Db       1 CAGTTTCCAGTCGGATGTCTACTCCTAT 28


RESULT 4
AR197894
LOCUS       AR197894                28 bp    DNA     linear   PAT 20-APR-2002
DEFINITION  Sequence 979 from patent US 6352829.
ACCESSION   AR197894
VERSION     AR197894.1  GI:20247743
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 28)
  AUTHORS   Chenchik,A., Jokhadze,G. and Bibilashvilli,R.
  TITLE     Methods of assaying differential expression
  JOURNAL   Patent: US 6352829-A 979 05-MAR-2002;
FEATURES             Location/Qualifiers
     source          1. .28
                     /organism="unknown"
BASE COUNT        5 a       8 c       5 g      10 t
ORIGIN

  Query Match             0.9%;  Score 28;  DB 6;  Length 28;
  Best Local Similarity   100.0%;  Pred. No. 2.7e+04;
  Matches   28;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy    1704 CAGTTTCCAGTCGGATGTCTACTCCTAT 1731
           ||||||||||||||||||||||||||||
Db       1 CAGTTTCCAGTCGGATGTCTACTCCTAT 28


RESULT 5
AR090860/c
LOCUS       AR090860                26 bp    DNA     linear   PAT 07-SEP-2000
DEFINITION  Sequence 980 from patent US 5994076.
ACCESSION   AR090860
VERSION     AR090860.1  GI:10017615
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 26)
  AUTHORS   Chenchik,A., Jokhadze,G. and Bibilashvilli,R.
  TITLE     Methods of assaying differential expression
  JOURNAL   Patent: US 5994076-A 980 30-NOV-1999;
FEATURES             Location/Qualifiers
     source          1. .26
                     /organism="unknown"
BASE COUNT        4 a       6 c       9 g       7 t
ORIGIN
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  Query Match             0.9%;  Score 26;  DB 6;  Length 26;
  Best Local Similarity   100.0%;  Pred. No. 1e+05;
  Matches   26;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy   1963 TCTCTACCGAAGATCAACCGGAGCGC 1988
          ||||||||||||||||||||||||||
Db     26 TCTCTACCGAAGATCAACCGGAGCGC 1


RESULT 6
AR197895/c
LOCUS       AR197895                  26 bp    DNA     linear   PAT 20-APR-2002
DEFINITION  Sequence 980 from patent US 6352829.
ACCESSION   AR197895
VERSION     AR197895.1  GI:20247744
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 26)
  AUTHORS   Chenchik,A., Jokhadze,G. and Bibilashvilli,R.
  TITLE     Methods of assaying differential expression
  JOURNAL   Patent: US 6352829-A 980 05-MAR-2002;
FEATURES             Location/Qualifiers
     source          1. .26
                     /organism="unknown"
BASE COUNT        4 a      6 c      9 g      7 t
ORIGIN

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  Best Local Similarity   100.0%;  Pred. No. 1e+05;
  Matches   26;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy   1963 TCTCTACCGAAGATCAACCGGAGCGC 1988
          ||||||||||||||||||||||||||
Db     26 TCTCTACCGAAGATCAACCGGAGCGC 1


RESULT 7
I96168/c
LOCUS       I96168                    26 bp    DNA     linear   PAT 01-DEC-1998
DEFINITION  Sequence 5 from patent US 5734039.
ACCESSION   I96168
VERSION     I96168.1  GI:3940638
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 26)
  AUTHORS   Calabretta,B. and Skorski,T.
  TITLE     Antisense oligonucleotides targeting cooperating oncogenes
  JOURNAL   Patent: US 5734039-A 5 31-MAR-1998;
FEATURES             Location/Qualifiers
     source          1. .26
                     /organism="unknown"
BASE COUNT        5 a      4 c     14 g      3 t
ORIGIN

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  Best Local Similarity   100.0%;  Pred. No. 1e+05;
  Matches   26;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      5 ATGTGACCGCCTCCCGCTCCCTCACC 30
          ||||||||||||||||||||||||||
Db     26 ATGTGACCGCCTCCCGCTCCCTCACC 1


RESULT 8
I96169
LOCUS       I96169                    26 bp    DNA     linear   PAT 01-DEC-1998
DEFINITION  Sequence 6 from patent US 5734039.
ACCESSION   I96169
VERSION     I96169.1  GI:3940639
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 26)
  AUTHORS   Calabretta,B. and Skorski,T.
  TITLE     Antisense oligonucleotides targeting cooperating oncogenes
  JOURNAL   Patent: US 5734039-A 6 31-MAR-1998;
FEATURES             Location/Qualifiers
     source          1. .26
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BASE COUNT        3 a      14 c      4 g      5 t
ORIGIN

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  Best Local Similarity   100.0%;  Pred. No. 1e+05;
  Matches   26;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      5 ATGTGACCGCCTCCCGCTCCCTCACC 30
          ||||||||||||||||||||||||||
Db      1 ATGTGACCGCCTCCCGCTCCCTCACC 26


RESULT 9
AR110776/c
LOCUS       AR110776                  25 bp    DNA     linear   PAT 14-FEB-2001
DEFINITION  Sequence 2 from patent US 6126965.
ACCESSION   AR110776
VERSION     AR110776.1  GI:12827624
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 25)
  AUTHORS   Kasid,U., Gokhale,P., Dritschilo,A. and Rahman,A.
  TITLE     Liposomes containing oligonucleotides
  JOURNAL   Patent: US 6126965-A 2 03-OCT-2000;
FEATURES             Location/Qualifiers
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BASE COUNT        4 a      7 c      6 g      8 t
ORIGIN

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  Best Local Similarity   100.0%;  Pred. No. 2e+05;
  Matches   25;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy    121 GCTGCATCAATGGAGCACATACAGG 145
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Db     25 GCTGCATCAATGGAGCACATACAGG 1


RESULT 10
AX157157/c
LOCUS       AX157157                  50 bp    DNA     linear   PAT 22-JUN-2001
DEFINITION  Sequence 485 from Patent WO0140521.
ACCESSION   AX157157
VERSION     AX157157.1  GI:14538488
KEYWORDS    .
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 50)
  AUTHORS   Shimkets,R.A. and Leach,M.
  TITLE     Nucleic acids containing single nucleotide polymorphisms and
            methods of use thereof
  JOURNAL   Patent: WO 0140521-A 485 07-JUN-2001;
            Curagen Corporation (US)
FEATURES             Location/Qualifiers
     source          1. .50
                     /organism="Homo sapiens"
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                     Accession number cg44928329"
     misc_feature    26
                     /note="1 of 2 allelic variants (486 is other entry)"
BASE COUNT       29 a      8 c      7 g      6 t
ORIGIN

  Query Match             0.7%;  Score 22.2;  DB 6;  Length 50;
  Best Local Similarity   77.1%;  Pred. No. 1.3e+06;
  Matches   27;  Conservative    0;  Mismatches    8;  Indels    0;  Gaps    0;

Qy   2875 TTCTTGATGATTTGGGTTTTAATTTTGTTTTTATT 2909
           ||||  |||||||||| |||  ||| ||| || ||
Db     50 TTCTCCATGATTTGGGGTTTTTTTTCGTTGTTGTT 16


RESULT 11
AR079693
LOCUS       AR079693                 43 bp    DNA     linear   PAT 31-AUG-2000
DEFINITION  Sequence 17 from patent US 5965726.
ACCESSION   AR079693
VERSION     AR079693.1  GI:10006434
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 43)
  AUTHORS   Pavlakis,G.N. and Felber,B.K.
  TITLE     Method of eliminating inhibitory/ instability regions of mRNA
  JOURNAL   Patent: US 5965726-A 17 12-OCT-1999;
FEATURES             Location/Qualifiers
     source          1. .43
                     /organism="unknown"
BASE COUNT       9 a      11 c      5 g      18 t
ORIGIN

  Query Match             0.7%;  Score 22;  DB 6;  Length 43;
  Best Local Similarity   73.7%;  Pred. No. 1.5e+06;
  Matches   28;  Conservative    0;  Mismatches   10;  Indels    0;  Gaps    0;

Qy   2207 TCACAGGGCCTTAACTTCATGTTGCCTTCTTTTCTATC 2244
           || |||   | || |||||| ||||||| || |||| |
Db      2 TCTCAGATACCTAGCTTCATATTGCCTTATTGTCTACC 39


RESULT 12
AR081223
LOCUS       AR081223                 43 bp    DNA     linear   PAT 31-AUG-2000
DEFINITION  Sequence 17 from patent US 5972596.
ACCESSION   AR081223
VERSION     AR081223.1  GI:10007949
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 43)
  AUTHORS   Pavlakis,G.N. and Felber,B.K.
  TITLE     Nucleic acid constructs containing HIV genes with mutated
            inhibitory/instability regions and methods of using same
  JOURNAL   Patent: US 5972596-A 17 26-OCT-1999;
FEATURES             Location/Qualifiers
     source          1. .43
                     /organism="unknown"
BASE COUNT       9 a      11 c      5 g      18 t
ORIGIN

  Query Match             0.7%;  Score 22;  DB 6;  Length 43;
  Best Local Similarity   73.7%;  Pred. No. 1.5e+06;
  Matches   28;  Conservative    0;  Mismatches   10;  Indels    0;  Gaps    0;

Qy   2207 TCACAGGGCCTTAACTTCATGTTGCCTTCTTTTCTATC 2244
           || |||   | || |||||| ||||||| || |||| |
Db      2 TCTCAGATACCTAGCTTCATATTGCCTTATTGTCTACC 39


RESULT 13
AR142002
LOCUS       AR142002                 43 bp    DNA     linear   PAT 08-AUG-2001
DEFINITION  Sequence 17 from patent US 6174666.
ACCESSION   AR142002
VERSION     AR142002.1  GI:15102302
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 43)
  AUTHORS   Pavlakis,G.N. and Felber,B.K.
  TITLE     Method of eliminating inhibitory/instability regions from mRNA
  JOURNAL   Patent: US 6174666-A 17 16-JAN-2001;
FEATURES             Location/Qualifiers
     source          1. .43
                     /organism="unknown"
BASE COUNT       9 a      11 c      5 g      18 t
ORIGIN

  Query Match             0.7%;  Score 22;  DB 6;  Length 43;
  Best Local Similarity   73.7%;  Pred. No. 1.5e+06;
  Matches   28;  Conservative    0;  Mismatches   10;  Indels    0;  Gaps    0;

Qy   2207 TCACAGGGCCTTAACTTCATGTTGCCTTCTTTTCTATC 2244
           || |||   | || |||||| ||||||| || |||| |
Db      2 TCTCAGATACCTAGCTTCATATTGCCTTATTGTCTACC 39


RESULT 14
AR170583
LOCUS       AR170583                 43 bp    DNA     linear   PAT 17-DEC-2001
DEFINITION  Sequence 17 from patent US 6291664.
ACCESSION   AR170583
VERSION     AR170583.1  GI:17908542
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 43)
  AUTHORS   Pavlakis,G.N. and Felber,B.K.
  TITLE     Method of eliminating inhibitory/instability regions of mRNA
  JOURNAL   Patent: US 6291664-A 17 18-SEP-2001;
FEATURES             Location/Qualifiers
     source          1. .43
                     /organism="unknown"
BASE COUNT       9 a      11 c      5 g      18 t
ORIGIN

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  Best Local Similarity   73.7%;  Pred. No. 1.5e+06;
  Matches   28;  Conservative    0;  Mismatches   10;  Indels    0;  Gaps    0;

Qy   2207 TCACAGGGCCTTAACTTCATGTTGCCTTCTTTTCTATC 2244
           || |||   | || |||||| ||||||| || |||| |
Db      2 TCTCAGATACCTAGCTTCATATTGCCTTATTGTCTACC 39


RESULT 15
AX164948/c
LOCUS       AX164948                 50 bp    DNA     linear   PAT 22-JUN-2001
DEFINITION  Sequence 143 from Patent WO0138586.
ACCESSION   AX164948
VERSION     AX164948.1  GI:14545777
KEYWORDS    .
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
```

```
REFERENCE   1  (bases 1 to 50)
  AUTHORS   Shimkets,R.A. and Leach,M.
  TITLE     Nucleic acids containing single nucleotide polymorphisms and
            methods of use thereof
  JOURNAL   Patent: WO 0138586-A 143 31-MAY-2001;
            Curagen Corporation (US)
FEATURES             Location/Qualifiers
     source          1. .50
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
     misc_feature    25. .26
                     /note="Nucleotide deleted between bases 25 and 26
                     Accession number cg43945210"
     variation       26
                     /note="single nucleotide polymorphism"
BASE COUNT        9 a     11 c      8 g     22 t
ORIGIN

  Query Match             0.7%;  Score 22;  DB 6;  Length 50;
  Best Local Similarity   83.3%;  Pred. No. 1.5e+06;
  Matches   25;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy    2804 AAACAAACAAACAAACAGCCTTGTTTCTCT 2833
           |||||||||||  ||| | ||||||  ||| |
Db      33 AAACAAACAAAAAAAGAACCTTGTGTCTGT 4


Search completed: May 16, 2003, 09:18:22
Job time : 7741 secs
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GenCore version 5.1.4_p5_4578

OM nucleic - nucleic search, using sw model

Run on: May 16, 2003, 05:00:24 ; Search time 629 Seconds
(without alignments)
10658.504 Million cell updates/sec

Title: US-10-057-550A-64
Perfect score: 2977
Sequence: 1 ccgaatgtgaccgcctcccg.....taataaaataaattaaattt 2977

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 2185239 seqs, 1125999159 residues

Total number of hits satisfying chosen parameters: 2166140

Minimum DB seq length: 0
Maximum DB seq length: 50

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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23: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA2001B.DAT:*
24: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA2002.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	35.6	1.2	42	21	AAA07016	Raf-1 mutagenic PC
	2	32.6	1.1	39	21	AAA07027	Raf-1 mutagenic PC
	3	32.4	1.1	42	21	AAA07017	Raf-1 mutagenic PC
	4	31	1.0	31	22	AAI30347	Human single nucle
	5	28	0.9	28	24	ABK66891	Human gene specifi
c	6	26	0.9	26	19	AAV20480	Human c-raf antise
c	7	26	0.9	26	24	ABK66892	Human gene specifi
c	8	26	0.9	50	22	AAL31396	Human SNP oligonuc
	9	25	0.8	25	22	AAH44455	Human latexin prot
c	10	24.2	0.8	35	21	AAA29996	Hairpin hybridizer
	11	24	0.8	24	19	AAV33096	C-raf probe 5. Sy
c	12	24	0.8	31	21	AAA30000	Hairpin hybridizer
c	13	24	0.8	33	21	AAA29998	Hairpin hybridizer
c	14	23	0.8	23	21	AAA26239	C-raf antisense ol
c	15	23	0.8	23	21	AAA26242	C-raf antisense ol
c	16	23	0.8	23	21	AAA26243	C-raf antisense ol
c	17	23	0.8	23	21	AAA26244	C-raf antisense ol
c	18	23	0.8	23	21	AAA26245	C-raf antisense ol
c	19	23	0.8	23	21	AAA26246	C-raf antisense ol
	20	22.4	0.8	27	22	AAH41610	Human c-Raf1 PCR p
	21	22.4	0.8	27	24	ABL50197	Human c-Raf1 PCR p
	22	22.4	0.8	27	24	ABL50229	Human c-Raf1 PCR p
c	23	22.4	0.8	50	22	AAL31673	Human SNP oligonuc
c	24	22.2	0.7	27	18	AAT93834	Phosphodiester oli
c	25	22.2	0.7	50	22	AAI73544	Human silent SNP c
c	26	22	0.7	30	22	AAH41590	Human c-Raf1 PCR p
c	27	22	0.7	30	24	ABL50177	Human c-Raf1 PCR p
c	28	22	0.7	30	24	ABL50209	Human c-Raf1 PCR p
	29	22	0.7	41	18	AAT93841	Phosphodiester oli
	30	22	0.7	43	14	AAQ50213	c-fos position 339
	31	22	0.7	47	21	AAZ69520	Human map-related
c	32	22	0.7	50	23	ABL00152	Human silent nonco
c	33	21.6	0.7	50	22	AAI75927	Human silent SNP c
	34	21.4	0.7	40	19	AAV05430	Primer RASSfiS use
	35	21.4	0.7	40	19	AAV05418	Primer used in pro
	36	21.4	0.7	40	21	AAA72878	Yeast RAF gene PCR
	37	21.4	0.7	40	21	AAA72893	Yeast PCR primer R
	38	21.4	0.7	40	21	AAA55851	RAF PCR primer SEQ
	39	21.4	0.7	40	21	AAA55866	GAD plasmid RAS in
	40	21.2	0.7	35	18	AAT93823	Antitumoural phosp
	41	21	0.7	21	22	AAF97098	Human gene single
	42	21	0.7	27	22	AAH41589	Human c-Raf1 PCR p
	43	21	0.7	27	24	ABL50176	Human c-Raf1 PCR p
	44	21	0.7	27	24	ABL50208	Human c-Raf1 PCR p
c	45	21	0.7	40	19	AAV05431	Primer RASSfiA use

ALIGNMENTS

RESULT 1
AAA07016
ID AAA07016 standard; DNA; 42 BP.
XX
AC AAA07016;
XX
DT 03-JUL-2000 (first entry)
XX
DE Raf-1 mutagenic PCR primer, SEQ ID NO:13.
XX
KW Raf-1; CAP kinase; phosphorylation; ceramide-activated protein kinase;
KW mutagenesis; lipopolysaccharide; LPS; endotoxin;
KW sphingomyelin signal transduction pathway; PCR primer; ss.
XX
OS Mammalia.
OS Synthetic.
XX
PN US6040149-A.
XX
PD 21-MAR-2000.
XX
PF 10-JAN-1997; 97US-0785247.
XX
PR 11-JAN-1996; 96US-0009900.
XX
PA (SLOK) SLOAN KETTERING INST CANCER RES.
XX
PI Zhang Y, Liu J, Kolesnick RN;
XX
DR WPI; 2000-270133/23.
XX
PT Novel method of identifying agents capable of inhibiting

PT lipopolysaccharide induced threonine phosphorylation by a
PT ceramide-activated protein kinase -
XX
PS Example VI; Column 56; 84pp; English.
XX
CC The invention relates to a novel method of determining whether an agent
CC is capable of specifically inhibiting the ability of a
CC ceramide-activated protein (CAP) kinase to phosphorylate the threonine
CC residue in a polypeptide containing a Thr-Pro- or Thr-Leu-Pro motif. In
CC particular, the peptide substrate that is specifically phosphorylated is
CC Raf-1, epidermal growth factor receptor (EGFR), or suitable fragments
CC thereof. The CAP kinase is membrane bound and has an apparent molecular
CC weight of 100-110 kD. It is an upstream participant in a sphingomyelin
CC signal transduction pathway which uses ceramide as a second messenger.
CC This pathway is initiated by tumour necrosis factor-alpha (TNF-alpha)
CC and interleukin-beta (IL-beta), causing the hydrolysis of sphingomyelin
CC to ceramide. The ceramide in turn stimulates the kinase to
CC phosphorylate protein substrates which can then mediate signal
CC transduction. The CAP kinase is also stimulated by the bacterial
CC endotoxin lipopolysaccharide (LPS), which is thought to mimic the second
CC messenger function of ceramide. The methods are useful for identifying
CC agents that inhibit lipopolysaccharide-induced Thr phosphorylation by
CC CAP kinase. The agents identified using the method are useful for
CC treating disorders associated with aberrant phosphorylation of target
CC molecules by CAP kinase, e.g., inflammatory disorders (such as rheumatoid
CC arthritis), ulcerative colitis, graft versus host disease, lupus
CC erythematosus, HIV, infection, disorders associated with poor stem cell
CC growth, and septic shock. Sequences AAA07016-A07019 and AAA07027
CC represent PCR primers used in an exemplification of the present invention
CC to generate mutant Flag peptide/Raf-1 sequences via overlap extension
CC PCR.
XX
SQ Sequence 42 BP; 9 A; 12 C; 14 G; 7 T; 0 other;

Query Match 1.2%; Score 35.6; DB 21; Length 42;
Best Local Similarity 90.5%; Pred. No. 1.4;
Matches 38; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 916 GTCCACATGGTCAGCACCACGCTGCCTGTGGACAGCAGGATG 957
||||||||||||||| |||||| || ||||||||||||||||
Db 1 GTCCACATGGTCAGCGTCACGCTACCGGTGGACAGCAGGATG 42

RESULT 2
AAA07027
ID AAA07027 standard; DNA; 39 BP.
XX
AC AAA07027;
XX
DT 03-JUL-2000 (first entry)
XX
DE Raf-1 mutagenic PCR primer, SEQ ID NO:27.
XX
KW Raf-1; CAP kinase; phosphorylation; ceramide-activated protein kinase;
KW mutagenesis; lipopolysaccharide; LPS; endotoxin;
KW sphingomyelin signal transduction pathway; PCR primer; ss.
XX
OS Mammalia.
OS Synthetic.
XX
PN US6040149-A.
XX
PD 21-MAR-2000.
XX
PF 10-JAN-1997; 97US-0785247.
XX
PR 11-JAN-1996; 96US-0009900.
XX
PA (SLOK) SLOAN KETTERING INST CANCER RES.
XX
PI Zhang Y, Liu J, Kolesnick RN;
XX
DR WPI; 2000-270133/23.

XX
PT Novel method of identifying agents capable of inhibiting
PT lipopolysaccharide induced threonine phosphorylation by a
PT ceramide-activated protein kinase -
XX
PS Example VI; Column 56; 84pp; English.
XX
CC The invention relates to a novel method of determining whether an agent
CC is capable of specifically inhibiting the ability of a
CC ceramide-activated protein (CAP) kinase to phosphorylate the threonine
CC residue in a polypeptide containing a Thr-Pro- or Thr-Leu-Pro motif. In
CC particular, the peptide substrate that is specifically phosphorylated is
CC Raf-1, epidermal growth factor receptor (EGFR), or suitable fragments
CC thereof. The CAP kinase is membrane bound and has an apparent molecular
CC weight of 100-110 kD. It is an upstream participant in a sphingomyelin
CC signal transduction pathway which uses ceramide as a second messenger.
CC This pathway is initiated by tumour necrosis factor-alpha (TNF-alpha)
CC and interleukin-beta (IL-beta), causing the hydrolysis of sphingomyelin
CC to ceramide. The ceramide in turn stimulates the kinase to
CC phosphorylate protein substrates which can then mediate signal
CC transduction. The CAP kinase is also stimulated by the bacterial
CC endotoxin lipopolysaccharide (LPS), which is thought to mimic the second
CC messenger function of ceramide. The methods are useful for identifying
CC agents that inhibit lipopolysaccharide-induced Thr phosphorylation by
CC CAP kinase. The agents identified using the method are useful for
CC treating disorders associated with aberrant phosphorylation of target
CC molecules by CAP kinase, e.g., inflammatory disorders (such as rheumatoid
CC arthritis), ulcerative colitis, graft versus host disease, lupus
CC erythematosus, HIV, infection, disorders associated with poor stem cell
CC growth, and septic shock. Sequences AAA07016-A07019 and AAA07027
CC represent PCR primers used in an exemplification of the present invention
CC to generate mutant Flag peptide/Raf-1 sequences via overlap extension
CC PCR.
XX
SQ Sequence 39 BP; 9 A; 11 C; 13 G; 6 T; 0 other;

Query Match 1.1%; Score 32.6; DB 21; Length 39;
Best Local Similarity 89.7%; Pred. No. 11;
Matches 35; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 919 CACATGGTCAGCACCACGCTGCCTGTGGACAGCAGGATG 957
||||||||||||||| ||| || ||||||||||||||||
Db 1 CACATGGTCAGCACCGTGCTACCGGTGGACAGCAGGATG 39

RESULT 3
AAA07017
ID AAA07017 standard; DNA; 42 BP.
XX
AC AAA07017;
XX
DT 03-JUL-2000 (first entry)
XX
DE Raf-1 mutagenic PCR primer, SEQ ID NO:14.
XX
KW Raf-1; CAP kinase; phosphorylation; ceramide-activated protein kinase;
KW mutagenesis; lipopolysaccharide; LPS; endotoxin;
KW sphingomyelin signal transduction pathway; PCR primer; ss.
XX
OS Mammalia.
OS Synthetic.
XX
PN US6040149-A.
XX
PD 21-MAR-2000.
XX
PF 10-JAN-1997; 97US-0785247.
XX
PR 11-JAN-1996; 96US-0009900.
XX
PA (SLOK) SLOAN KETTERING INST CANCER RES.
XX
PI Zhang Y, Liu J, Kolesnick RN;

XX
DR WPI; 2000-270133/23.
XX
PT Novel method of identifying agents capable of inhibiting
PT lipopolysaccharide induced threonine phosphorylation by a
PT ceramide-activated protein kinase -
XX
PS Example VI; Column 56; 84pp; English.
XX
CC The invention relates to a novel method of determining whether an agent
CC is capable of specifically inhibiting the ability of a
CC ceramide-activated protein (CAP) kinase to phosphorylate the threonine
CC residue in a polypeptide containing a Thr-Pro- or Thr-Leu-Pro motif. In
CC particular, the peptide substrate that is specifically phosphorylated is
CC Raf-1, epidermal growth factor receptor (EGFR), or suitable fragments
CC thereof. The CAP kinase is membrane bound and has an apparent molecular
CC weight of 100-110 kD. It is an upstream participant in a sphingomyelin
CC signal transduction pathway which uses ceramide as a second messenger.
CC This pathway is initiated by tumour necrosis factor-alpha (TNF-alpha)
CC and interleukin-beta (IL-beta), causing the hydrolysis of sphingomyelin
CC to ceramide. The ceramide in turn stimulates the kinase to
CC phosphorylate protein substrates which can then mediate signal
CC transduction. The CAP kinase is also stimulated by the bacterial
CC endotoxin lipopolysaccharide (LPS), which is thought to mimic the second
CC messenger function of ceramide. The methods are useful for identifying
CC agents that inhibit lipopolysaccharide-induced Thr phosphorylation by
CC CAP kinase. The agents identified using the method are useful for
CC treating disorders associated with aberrant phosphorylation of target
CC molecules by CAP kinase, e.g., inflammatory disorders (such as rheumatoid
CC arthritis), ulcerative colitis, graft versus host disease, lupus
CC erythematosus, HIV, infection, disorders associated with poor stem cell
CC growth, and septic shock. Sequences AAA07016-A07019 and AAA07027
CC represent PCR primers used in an exemplification of the present invention
CC to generate mutant Flag peptide/Raf-1 sequences via overlap extension
CC PCR.
XX
SQ Sequence 42 BP; 8 A; 11 C; 15 G; 8 T; 0 other;

Query Match 1.1%; Score 32.4; DB 21; Length 42;
Best Local Similarity 85.7%; Pred. No. 13;
Matches 36; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 916 GTCCACATGGTCAGCACCACGCTGCCTGTGGACAGCAGGATG 957
||||||||||||||| | ||| || ||||||||||||||||
Db 1 GTCCACATGGTCAGCGTCGTGCTACCGGTGGACAGCAGGATG 42

RESULT 4
AAI30347
ID AAI30347 standard; DNA; 31 BP.
XX
AC AAI30347;
XX
DT 18-OCT-2001 (first entry)
XX
DE Human single nucleotide polymorphism (SNP) RAF1.
XX
KW Human; resequence; genotype; disease; forensic; paternity testing;
KW single nucleotide polymorphism; SNP; ss.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Variation replace(16,T)
FT /*tag= a
FT /standard_name= "single nucleotide polymorphism"
XX
PN WO200166800-A2.
XX
PD 13-SEP-2001.
XX
PF 07-MAR-2001; 2001WO-US07268.
XX
PR 07-MAR-2000; 2000US-0187510.
PR 22-MAY-2000; 2000US-0206129.
XX
PA (WHED) WHITEHEAD INST BIOMEDICAL RES.
XX
PI Cargill M, Ireland JS, Lander ES;
XX
DR WPI; 2001-522952/57.
XX
PT Nucleic acid molecules from the human genome which include polymorphic
PT sites, useful in methods for predicting the presence, absence or
PT severity of a particular phenotype or disorder (e.g. diabetes)
PT associated with a particular genotype -
XX
PS Claim 1; Page 80; 145pp; English.
XX
CC The invention relates to the identification of nucleic acid molecules
CC (AAI29513-AAI31314) from the human genome which include polymorphic sites
CC which can predispose individuals to disease. Various genes from a number
CC of individuals were resequenced and single nucleotide polymorphisms
CC (SNPs) in these genes discovered. The method is useful for predicting the
CC presence, absence or severity of a particular phenotype or disorder (e.g.
CC diabetes) associated with a particular genotype. The nucleic acids
CC containing the polymorphic sites may be useful in forensics and paternity
CC testing.
XX
SQ Sequence 31 BP; 7 A; 10 C; 5 G; 9 T; 0 other;

Query Match 1.0%; Score 31; DB 22; Length 31;
Best Local Similarity 100.0%; Pred. No. 29;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2144 CCCTTTCTCCAGAGGCAGAACACATGTTTTC 2174
|||||||||||||||||||||||||||||||
Db 1 CCCTTTCTCCAGAGGCAGAACACATGTTTTC 31

RESULT 5
ABK66891
ID ABK66891 standard; DNA; 28 BP.
XX
AC ABK66891;
XX
DT 02-JUL-2002 (first entry)
XX
DE Human gene specific PCR primer #979.
XX
KW Primer; ss; DNA microarray; differential expression analysis; human.
XX
OS Homo sapiens.
XX
PN US6352829-B1.
XX
PD 05-MAR-2002.
XX
PF 05-JAN-1999; 99US-0225928.
XX
PR 21-MAY-1997; 97US-0859998.
XX
PA (CLON-) CLONTECH LAB INC.
XX
PI Chenchik A, Jokhadze G, Bibilashvilli R;
XX
DR WPI; 2002-314699/35.
XX
PT Producing sub-population of labeled nucleic acids, useful for analysing
PT differences in RNA profiles between several different physiological
PT sources, using set of distinct gene specific primers -
XX
PS Example 3; SEQ ID No 979; 11pp; English.
XX
CC The invention relates to producing a sub-population of labeled nucleic
CC acids (NAs) comprising contacting a NA sample from a physiological

```
CC   source, with a pool of 50 distinct gene specific primers under suitable
CC   conditions to enzymatically generate sub-population of NAs, where
CC   each gene specific primer has a sequence complementary to a distinct
CC   mRNA, and each labeled NA is generated using a single gene specific
CC   primer. The method is useful for producing a sub-population of labeled
CC   NAs which is useful for analysing the differences in the RNA profiles
CC   between several different physiological sources, where the method
CC   comprises producing subpopulation of labeled NAs for the different
CC   physiological sources, comprising the populations for each physiological
CC   source to identify differences in the population, where the comparison
CC   is preferably performed by hybridising the labeled NAs for each of the
CC   distinct physiological sources to an array of probe NAs stably
CC   associated with the surface of a substrate to produce a hybridisation
CC   pattern for each of the sources, and comparing the patterns for each of
CC   the sources, where differential gene expression assays are
CC   utilised in differential expression analysis of diseased a normal
CC   tissue e.g. neoplastic a normal tissue, or different tissue or
CC   subtissue types. The present sequence is a human gene specific PCR
CC   primer used in the method of the invention.
CC   Note: The sequence data for this patent did not form part
CC   of the printed specification, but was obtained in electronic
CC   format directly from USPTO at
CC   http.wipo.seqdata.uspto.gov/sequence.html?DocID=6352829B1.
XX
SQ   Sequence 28 BP; 5 A; 8 C; 5 G; 10 T; 0 other;

  Query Match             0.9%;  Score 28;  DB 24;  Length 28;
  Best Local Similarity   100.0%;  Pred. No. 2.2e+02;
  Matches   28;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy    1704 CAGTTTCCAGTCGGATGTCTACTCCTAT 1731
           ||||||||||||||||||||||||||||
Db       1 CAGTTTCCAGTCGGATGTCTACTCCTAT 28


RESULT 6
AAV20480/c
ID   AAV20480 standard; DNA; 26 BP.
XX
AC   AAV20480;
XX
DT   17-JUN-1998  (first entry)
XX
DE   Human c-raf antisense oligonucleotide.
XX
KW   Human; oncogene; proto-oncogene; neoplastic disease; anticancer;
KW   cancer; antisense oligonucleotide; phosphorothioate; ss.
XX
OS   Synthetic.
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   allele          1..26
FT                   /*tag=  a
FT                   /note= "phosphorothioate linkages"
XX
PN   US5734039-A.
XX
PD   31-MAR-1998.
XX
PF   15-SEP-1994;   94US-0306691.
XX
PR   15-SEP-1994;   94US-0306691.
XX
PA   (UYJE-) UNIV JEFFERSON THOMAS.
XX
PI   Calabretta B,  Skorski T;
XX
DR   WPI; 1998-229882/20.
XX
PT   Anticancer composition comprising two anti-sense oligo:nucleotide(s)
PT    - targetting cytoplasmic and nuclear oncogene(s)
XX
PS   Example 4; Column 33; 92pp; English.
XX
CC   The present sequence represents an antisense oligonucleotide from the
CC   present invention. The present invention describes a composition which
CC   comprises two antisense oligonucleotides. The first oligonucleotide is
CC   specific for a cytoplasmic oncogene or proto-oncogene selected from
CC   ras, raf, EGF-1, c-fms, c-ros, c-kit, c-met, c-trk, c-src, c-abl,
CC   bcr-abl, c-fgr and c-yes. The second oligonucleotide is specific for a
CC   nuclear oncogene or proto-oncogene selected from myc, jun, c-ets,
CC   c-fos, c-myb, B-myb, c-rel, c-vav, c-ski, c-spi, cyclin D1, PML/RAR
CC   alpha , AML1/MTG8, E2A/prl and ALL-1/AF-4. The composition is used for
CC   treating cancer. The combination of antisense oligonucleotides has
CC   synergistically enhanced ability to inhibit growth of cancer cells.
XX
SQ   Sequence 26 BP; 5 A; 4 C; 14 G; 3 T; 0 other;

  Query Match             0.9%;  Score 26;  DB 19;  Length 26;
  Best Local Similarity   100.0%;  Pred. No. 8.6e+02;
  Matches   26;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       5 ATGTGACCGCCTCCCGCTCCCTCACC 30
           ||||||||||||||||||||||||||
Db      26 ATGTGACCGCCTCCCGCTCCCTCACC 1


RESULT 7
ABK66892/c
ID   ABK66892 standard; DNA; 26 BP.
XX
AC   ABK66892;
XX
DT   02-JUL-2002  (first entry)
XX
DE   Human gene specific PCR primer  #980.
XX
KW   Primer; ss; DNA microarray; differential expression analysis; human.
XX
OS   Homo sapiens.
XX
PN   US6352829-B1.
XX
PD   05-MAR-2002.
XX
PF   05-JAN-1999;   99US-0225928.
XX
PR   21-MAY-1997;   97US-0859998.
XX
PA   (CLON-) CLONTECH LAB INC.
XX
PI   Chenchik A,  Jokhadze G,  Bibilashvilli R;
XX
DR   WPI; 2002-314699/35.
XX
PT   Producing sub-population of labeled nucleic acids, useful for analysing
PT   differences in RNA profiles between several different physiological
PT   sources, using set of distinct gene specific primers  -
XX
PS   Example 3; SEQ ID No 980; 11pp; English.
XX
CC   The invention relates to producing a sub-population of labeled nucleic
CC   acids (NAs) comprising contacting a NA sample from a physiological
CC   source, with a pool of 50 distinct gene specific primers under suitable
CC   conditions to enzymatically generate sub-population of NAs, where
CC   each gene specific primer has a sequence complementary to a distinct
CC   mRNA, and each labeled NA is generated using a single gene specific
CC   primer. The method is useful for producing a sub-population of labeled
CC   NAs which is useful for analysing the differences in the RNA profiles
CC   between several different physiological sources, where the method
CC   comprises producing subpopulation of labeled NAs for the different
CC   physiological sources, comprising the populations for each physiological
CC   source to identify differences in the population, where the comparison
CC   is preferably performed by hybridising the labeled NAs for each of the
CC   distinct physiological sources to an array of probe NAs stably
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CC   associated with the surface of a substrate to produce a hybridisation
CC   pattern for each of the sources, and comparing the patterns for each of
CC   the sources, where differential gene expression assays are
CC   utilised in differential expression analysis of diseased a normal
CC   tissue e.g. neoplastic a normal tissue, or different tissue or
CC   subtissue types. The present sequence is a human gene specific PCR
CC   primer used in the method of the invention.
CC   Note: The sequence data for this patent did not form part
CC   of the printed specification, but was obtained in electronic
CC   format directly from USPTO at
CC   http.wipo.seqdata.uspto.gov/sequence.html?DocID=6352829B1.
XX
SQ   Sequence 26 BP; 4 A; 6 C; 9 G; 7 T; 0 other;

  Query Match             0.9%;  Score 26;  DB 24;  Length 26;
  Best Local Similarity   100.0%;  Pred. No. 8.6e+02;
  Matches   26;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy    1963 TCTCTACCGAAGATCAACCGGAGCGC 1988
           ||||||||||||||||||||||||||
Db      26 TCTCTACCGAAGATCAACCGGAGCGC 1

RESULT 8
AAL31396/c
ID   AAL31396 standard; DNA; 50 BP.
XX
AC   AAL31396;
XX
DT   24-JAN-2002  (first entry)
XX
DE   Human SNP oligonucleotide #4604.
XX
KW   Immunosuppressive; immunostimulatory; antiinflammatory; cytostatic;
KW   neuroprotective; antimicrobial; gene therapy; vaccine; amylase; cancer;
KW   amyloid protein; angiopoietin; apoptosis related protein; cadherin;
KW   cyclin; polymerase; oncogene; histone; kinase; colony stimulating factor;
KW   complement related protein; cytochrome; kinesin; cytokine; interferon;
KW   interleukin; G-protein coupled receptor; thioesterase; inflammation;
KW   multifactorial disease; autoimmune disease; infection;
KW   nervous system disease; ss.
XX
OS   Homo sapiens.
XX
PN   WO200147944-A2.
XX
PD   05-JUL-2001.
XX
PF   28-DEC-2000; 2000WO-US35498.
XX
PR   28-DEC-1999;   99US-0173419.
PR   27-DEC-2000; 2000US-0173419.
XX
PA   (CURA-) CURAGEN CORP.
XX
PI   Shimkets RA,  Leach M;
XX
DR   WPI; 2001-465210/50.
XX
PT   Polymorphic nucleic acids encoding e.g. amylases, cyclins, polymerases,
PT   oncogenes and histones, useful for diagnosing and treating, e.g.
PT   cancer, autoimmune diseases and infections -
XX
PS   Claim 1; Page 2710; 4143pp; English.
XX
CC   The present invention relates to oligonucleotides encoding polymorphic
CC   variants of proteins related to amylases, amyloid proteins, angiopoietin,
CC   apoptosis related proteins, cadherin, cyclin, polymerase, oncogenes,
CC   histones, kinases, colony stimulating factors, complement related
CC   proteins, cytochromes, kinesins, cytokines, interferons, interleukins,
CC   G-protein coupled receptors and thioesterases. The present sequence is
CC   one such oligonucleotide. The oligonucleotides and the peptides encoded
CC   by them may be used in the prevention, diagnosis and treatment of
CC   diseases associated with inappropriate expression of the proteins listed
CC   above. Disorders that may be prevented, diagnosed and/or treated include
CC   multifactorial diseases with a genetic component, such as autoimmune
CC   diseases (e.g. rheumatoid arthritis, multiple sclerosis, diabetes,
CC   systemic lupus erythromatosus and Grave's disease), inflammation, cancer
CC   (e.g. cancers of the bladder, brain, breast, colon and kidney;
CC   leukaemia), diseases of the nervous system and an infection of pathogenic
CC   organisms.
XX
SQ   Sequence 50 BP; 5 A; 8 C; 9 G; 28 T; 0 other;

  Query Match             0.9%;  Score 26;  DB 22;  Length 50;
  Best Local Similarity   70.0%;  Pred. No. 1.3e+03;
  Matches   35;  Conservative    0;  Mismatches   15;  Indels    0;  Gaps    0;

Qy    2775 GGGCCGCAGGGCCAGCCTGTTTCTCTAACAAACAAACAAACAAACAGCCT 2824
           ||||  ||| || || ||   |||| || ||| ||| ||| ||| ||| |
Db      50 GGGCAACAGAGCAAGACTCCGTCTCAAAAAAAAAAAAAAAAAAAAAGCTT 1

RESULT 9
AAH44455
ID   AAH44455 standard; DNA; 25 BP.
XX
AC   AAH44455;
XX
DT   12-OCT-2001  (first entry)
XX
DE   Human latexin protein 46 PCR primer 2 SEQ ID NO:4.
XX
KW   Human; latexin protein 46; cytostatic; antiviral; anti-HIV;
KW   immunomodulatory; antiinflammatory; diagnosis; malignant tumour;
KW   haemopathy; HIV infection; immunological disease; inflammation;
KW   PCR primer; ss.
XX
OS   Homo sapiens.
XX
PN   WO200149737-A1.
XX
PD   12-JUL-2001.
XX
PF   25-DEC-2000; 2000WO-CN00664.
XX
PR   29-DEC-1999;   99CN-0127234.
XX
PA   (UYFU-) UNIV FUDAN.
PA   (SHAN-) SHANGHAI BIO DOOR GENE TECHNOLOGY LTD.
XX
PI   Mao Y,  Xie Y;
XX
DR   WPI; 2001-432872/46.
XX
PT   Human latexin protein 46 and encoded polynucleotide, applicable in
PT   diagnosis and treatment of malignant tumor, hemopathy, HIV infection,
PT   immunological diseases and inflammation -
XX
PS   Example 3; Page 18; 39pp; Chinese.
XX
CC   The present invention describes human latexin protein 46 (I). (I) has
CC   cytostatic, antiviral, anti-HIV, immunomodulatory and antiinflammatory
CC   activities. (I) and the polynucleotide encoding it are applicable in
CC   the diagnosis and treatment of malignant tumour, haemopathy, HIV
CC   infection, immunological diseases and various inflammations. The present
CC   sequence represents a PCR primer for human latexin protein 46, which is
CC   used in an example from the present invention.
XX
SQ   Sequence 25 BP; 3 A; 0 C; 5 G; 17 T; 0 other;

  Query Match             0.8%;  Score 25;  DB 22;  Length 25;
  Best Local Similarity   100.0%;  Pred. No. 1.7e+03;
  Matches   25;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy    2882 TGATTTGGGTTTTAATTTTGTTTTT 2906
```

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                    ||||||||||||||||||||||||
Db      1 TGATTTGGGTTTTAATTTTGTTTTT 25

RESULT 10
AAA29996/c
ID   AAA29996 standard; DNA; 35 BP.
XX
AC   AAA29996;
XX
DT   09-AUG-2000  (first entry)
XX
DE   Hairpin hybridizer molecule #1 targeting c-raf RNA.
XX
KW   DNA-RNA hybrid; phosphorothioate; hairpin hybridizer molecule; HPH;
KW   c-raf; inhibitor; detect; nuclease resistance; gene function;
KW   gene expression modulator; ss.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   stem_loop       1..35
FT                   /*tag=  a
FT   misc_RNA        1..13
FT                   /*tag=  b
FT                   /note= "2'-O-methyl-ribonucleotides"
FT   misc_feature    1..4
FT                   /*tag=  c
FT                   /note= "Phosphorothioate internucleotide linkage"
FT   misc_feature    14..23
FT                   /*tag=  d
FT                   /note= "Phosphorothioate internucleotide linkage"
FT   misc_RNA        23..35
FT                   /*tag=  e
FT                   /note= "2'-O-methyl-ribonucleotides"
FT   misc_feature    32..35
FT                   /*tag=  f
FT                   /note= "Phosphorothioate internucleotide linkage"
XX
PN   WO200017346-A2.
XX
PD   30-MAR-2000.
XX
PF   20-SEP-1999;   99WO-US21865.
XX
PR   21-SEP-1998;   98US-0101174.
XX
PA   (RIBO-) RIBOZYME PHARM INC.
XX
PI   Hartmann T, Zwick M,  Thompson J,  Jarvis T;
XX
DR   WPI; 2000-292841/25.
XX
PT   Modulating target sequence in a cell, useful e.g. therapeutically or
PT   for identifying gene function, by treatment with novel hairpin
PT   hybridizer nucleic acid molecules -
XX
PS   Claim 46; Page 76; 128pp; English.
XX
CC   A method for modulating the function of a target sequence in a cell
CC   comprises treatment with a hairpin hybridizer (HPH) nucleic acid molecule
CC   such as that represented by the present sequence. The present HPH
CC   molecule is used in an example of the invention and targets the human
CC   c-raf gene. The HPH molecules function through RNA/DNA inhibition. The
CC   HPH molecule binds to and blocks the function of a target nucleic acid,
CC   and modulated cellular and viral processes such as splicing, editing, and
CC   translation. The HPH molecule can be used therapeutically, in target
CC   validation, to identify gene function and/or therapeutic targets, for
CC   analysis of mutations in diseased cell and to detect specific RNA. The
CC   hairpin structure improves resistance to nuclease degradation,
CC   localization within the cell, and uptake by cells. The HPH may include a
CC   sequence that activates RNase H (for cleaving RNA) and its specificity is
CC   greater than for linear antisense sequences.
XX
SQ   Sequence 35 BP; 6 A; 9 C; 13 G; 1 T; 6 U; 0 other;

  Query Match             0.8%;  Score 24.2;  DB 21;  Length 35;
  Best Local Similarity   89.7%;  Pred. No. 3.7e+03;
  Matches   26;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy    2029 ATCAATGCTTGCACGCTGACCACGTCCCC 2057
           ||||||||||||||||||||||||||  | |
Db      29 ATCAATGCTTGCACGCTGACCACGCTCGC 1


RESULT 11
AAV33096
ID   AAV33096 standard; DNA; 24 BP.
XX
AC   AAV33096;
XX
DT   18-NOV-1998  (first entry)
XX
DE   C-raf probe 5.
XX
KW   Multiplex competitive PCR reaction; MC-PCR; reverse-transcriptase PCR;
KW   RT-PCR; tagging reaction; competitive amplification reaction;
KW   probe; housekeeping gene; C-raf; hybridisation; ss.
XX
OS   Synthetic.
OS   Homo sapiens.
XX
PN   WO9835058-A2.
XX
PD   13-AUG-1998.
XX
PF   27-JAN-1998;   98WO-US01471.
XX
PR   07-FEB-1997;   97US-0037841.
XX
PA   (RIBO-) RIBOZYME PHARM INC.
XX
PI   Thompson JD;
XX
DR   WPI; 1998-447252/38.
XX
PT   Determining relative amounts of different nucleic acids by multiplex
PT   competitive polymerase chain reaction - involves tagging target and
PT   control sequences then amplification with generic primer pair
PT   corresponding to tagging sequences, used e.g. to determine response
PT   to drugs
XX
PS   Example 1; Page 22; 45pp; English.
XX
CC   The present invention provides a method for determining the
CC   relative amounts of two or more different nucleic acid molecules
CC   by using the multiplex competitive PCR reaction (MC-PCR).  A MC-PCR
CC   reaction involves a reverse-transcriptase (RT-PCR) reaction followed
CC   by a tagging reaction and a competitive amplification reaction.  The
CC   RT-PCR reaction uses a primer #2 to convert target mRNA into cDNA.
CC   Primer #1 in combination with primer #2 is then used to convert
CC   the region of the resulting cDNA to be amplified during the MC-PCR
CC   reaction into a double-stranded molecule.  Primers #3 and #4, nested
CC   relative to primers #1 and #2 respectively, are used as tagging
CC   primers in the tagging reaction.  A forward tagging primer has a
CC   defined sequence at its 5' end (+TAG sequence) while a reverse
CC   tagging primer has a different defined sequence at its 3' end (-TAG
CC   sequence).  The purpose of the tagging reaction is to introduce the
CC   two defined sequences at the correct ends of the sequence to be
CC   amplified.  The competitive amplification reaction involves using a
CC   single pair of generic primers, whose sequences are complementary to
CC   the +TAG and -TAG sequences, to amplify the different products
CC   generated from the cDNAs during the tagging step.  This amplification
CC   reaction is competitive due to the use of a single primer pair to
CC   amplify the different target RNAs.  Probe #5, complementary to the
CC   region of target RNA being amplified, is used to specifically detect
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CC   the amplified product.  The MC-PCR reaction can amplify one or more
CC   target mRNAs in a sample using the primer set #1-#5 for each target
CC   mRNA.  In the example given, primers #1, #2, #3, #4 and probe #5
CC   are the C-raf primers 1 (AAV33092), 2 (AAV33093), 3 (AAV33094), 4
CC   (AAV33095) and probe 5 respectively.  These primers/probes were used to
CC   illustrate the method of the invention.  The method claims to allow
CC   detection of low-abundance mRNA in small samples (e.g. 10 ng is
CC   sufficient) with high precision, and uses housekeeping genes as controls
CC   for RNA input and integrity.  Also, a large number of samples may be
CC   processed simultaneously, making the process suitable for high
CC   throughput screening, and does not require continuous monitoring.
XX
SQ   Sequence 24 BP; 7 A; 9 C; 3 G; 5 T; 0 other;

  Query Match             0.8%;  Score 24;  DB 19;  Length 24;
  Best Local Similarity   100.0%;  Pred. No. 3.3e+03;
  Matches   24;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy    816 GCACAGATATTCTACACCTCACGC 839
          ||||||||||||||||||||||||
Db      1 GCACAGATATTCTACACCTCACGC 24


RESULT 12
AAA30000/c
ID   AAA30000 standard; DNA; 31 BP.
XX
AC   AAA30000;
XX
DT   09-AUG-2000  (first entry)
XX
DE   Hairpin hybridizer molecule #5 targeting c-raf RNA.
XX
KW   DNA-RNA hybrid; phosphorothioate; hairpin hybridizer molecule; HPH;
KW   c-raf; inhibitor; detect; nuclease resistance; gene function;
KW   gene expression modulator; ss.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   stem_loop       1..31
FT                   /*tag=  a
FT   misc_RNA        1..11
FT                   /*tag=  b
FT                   /note= "2'-O-methyl-ribonucleotides"
FT   misc_feature    1..4
FT                   /*tag=  c
FT                   /note= "Phosphorothioate internucleotide linkage"
FT   misc_feature    12..20
FT                   /*tag=  d
FT                   /note= "Phosphorothioate internucleotide linkage"
FT   misc_RNA        21..31
FT                   /*tag=  e
FT                   /note= "2'-O-methyl-ribonucleotides"
FT   misc_feature    28..31
FT                   /*tag=  f
FT                   /note= "Phosphorothioate internucleotide linkage"
XX
PN   WO200017346-A2.
XX
PD   30-MAR-2000.
XX
PF   20-SEP-1999;   99WO-US21865.
XX
PR   21-SEP-1998;   98US-0101174.
XX
PA   (RIBO-) RIBOZYME PHARM INC.
XX
PI   Hartmann T,  Zwick M,  Thompson J,  Jarvis T;
XX
DR   WPI; 2000-292841/25.
XX
PT   Modulating target sequence in a cell, useful e.g. therapeutically or
PT   for identifying gene function, by treatment with novel hairpin
PT   hybridizer nucleic acid molecules
XX
PS   Claim 3; Page 76; 128pp; English.
XX
CC   A method for modulating the function of a target sequence in a cell
CC   comprises treatment with a hairpin hybridizer (HPH) nucleic acid molecule
CC   such as that represented by the present sequence. The present HPH
CC   molecule is used in an example of the invention and targets the human
CC   c-raf gene. The HPH molecules function through RNA/DNA inhibition. The
CC   HPH molecule binds to and blocks the function of a target nucleic acid,
CC   and modulated cellular and viral processes such as splicing, editing, and
CC   translation. The HPH molecule can be used therapeutically, in target
CC   validation, to identify gene function and/or therapeutic targets, for
CC   analysis of mutations in diseased cell and to detect specific RNA. The
CC   hairpin structure improves resistance to nuclease degradation,
CC   localization within the cell, and uptake by cells. The HPH may include a
CC   sequence that activates RNase H (for cleaving RNA) and its specificity is
CC   greater than for linear antisense sequences.
XX
SQ   Sequence 31 BP; 6 A; 7 C; 11 G; 1 T; 6 U; 0 other;

  Query Match             0.8%;  Score 24;  DB 21;  Length 31;
  Best Local Similarity   100.0%;  Pred. No. 3.9e+03;
  Matches   24;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy   2029 ATCAATGCTTGCACGCTGACCACG 2052
           ||||||||||||||||||||||||
Db     27 ATCAATGCTTGCACGCTGACCACG 4


RESULT 13
AAA29998/c
ID   AAA29998 standard; DNA; 33 BP.
XX
AC   AAA29998;
XX
DT   09-AUG-2000  (first entry)
XX
DE   Hairpin hybridizer molecule #3 targeting c-raf RNA.
XX
KW   DNA-RNA hybrid; phosphorothioate; hairpin hybridizer molecule; HPH;
KW   c-raf; inhibitor; detect; nuclease resistance; gene function;
KW   gene expression modulator; ss.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   stem_loop       1..33
FT                   /*tag=  a
FT   misc_RNA        1..12
FT                   /*tag=  b
FT                   /note= "2'-O-methyl-ribonucleotides"
FT   misc_feature    1..4
FT                   /*tag=  c
FT                   /note= "Phosphorothioate internucleotide linkage"
FT   misc_feature    13..21
FT                   /*tag=  d
FT                   /note= "Phosphorothioate internucleotide linkage"
FT   misc_RNA        22..33
FT                   /*tag=  e
FT                   /note= "2'-O-methyl-ribonucleotides"
FT   misc_feature    30..33
FT                   /*tag=  f
FT                   /note= "Phosphorothioate internucleotide linkage"
XX
PN   WO200017346-A2.
XX
PD   30-MAR-2000.
XX
PF   20-SEP-1999;   99WO-US21865.
XX
PR   21-SEP-1998;   98US-0101174.
```

```
XX
PA   (RIBO-) RIBOZYME PHARM INC.
XX
PI   Hartmann T,  Zwick M,  Thompson J,  Jarvis T;
XX
DR   WPI; 2000-292841/25.
XX
PT   Modulating target sequence in a cell, useful e.g. therapeutically or
PT   for identifying gene function, by treatment with novel hairpin
PT   hybridizer nucleic acid molecules -
XX
PS   Claim 44; Page 76; 128pp; English.
XX
CC   A method for modulating the function of a target sequence in a cell
CC   comprises treatment with a hairpin hybridizer (HPH) nucleic acid molecule
CC   such as that represented by the present sequence. The present HPH
CC   molecule is used in an example of the invention and targets the human
CC   c-raf gene. The HPH molecules function through RNA/DNA inhibition. The
CC   HPH molecule binds to and blocks the function of a target nucleic acid,
CC   and modulated cellular and viral processes such as splicing, editing, and
CC   translation. The HPH molecule can be used therapeutically, in target
CC   validation, to identify gene function and/or therapeutic targets, for
CC   analysis of mutations in diseased cell and to detect specific RNA. The
CC   hairpin structure improves resistance to nuclease degradation,
CC   localization within the cell, and uptake by cells. The HPH may include a
CC   sequence that activates RNase H (for cleaving RNA) and its specificity is
CC   greater than for linear antisense sequences.
XX
SQ   Sequence 33 BP; 6 A; 8 C; 12 G; 1 T; 6 U; 0 other;

  Query Match             0.8%;  Score 24;  DB 21;  Length 33;
  Best Local Similarity   100.0%;  Pred. No. 4.1e+03;
  Matches   24;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy    2029 ATCAATGCTTGCACGCTGACCACG 2052
           ||||||||||||||||||||||||
Db      28 ATCAATGCTTGCACGCTGACCACG 5


RESULT 14
AAA26239/c
ID   AAA26239 standard; DNA; 23 BP.
XX
AC   AAA26239;
XX
DT   19-JUL-2000  (first entry)
XX
DE   C-raf antisense oligonucleotide sequence SEQ ID NO:2737.
XX
KW   Oestrogen receptor; c-raf; k-ras; bcl-2; ribozyme; cleavage;
KW   hammerhead ribozyme; hairpin ribozyme; antisense oligonucleotide;
KW   gene expression modification; cancer; phosphorothioate; endonuclease;
KW   anticancer; breast cancer; endometrium cancer; ss.
XX
OS   Homo sapiens.
XX
PN   WO9954459-A2.
XX
PD   28-OCT-1999.
XX
PF   19-APR-1999;   99WO-US08547.
XX
PR   20-APR-1998;   98US-0082404.
PR   23-JUN-1998;   98US-0103636.
XX
PA   (RIBO-) RIBOZYME PHARM INC.
XX
PI   Thompson JD,  Beigelman L,  McSwiggen JA,  Karpeisky A,  Bellon L;
PI   Reynolds M,  Zwick M,  Jarvis T,  Woolf T,  Haeberli P;
PI   Matulic-Adamic J;
XX
DR   WPI; 2000-013248/01.
XX
PT   New nucleic acids that interact, and optionally cleave, target
PT   sequences, used to treat cancer -
XX
PS   Example 8; Page 105; 148pp; English.
XX
CC   The present invention describes nucleic acids (A) that interact stably
CC   with a target sequence and contain at least one phosphoro(di)thioate
CC   link, having endonuclease activity. (A), and more generally any
CC   catalytic nucleic acid (A') that modulates expression of the oestrogen
CC   receptor gene, are used to treat cancer (particularly of breast or
CC   endometrium), in vivo or by transforming cells ex vivo and implanting
CC   treated cells, or for other conditions associated with levels of
CC   oestrogen receptor. Because of the high selectivity for targeted RNA, (A)
CC   can also be used to correlate inhibition of gene expression with
CC   alterations in phenotype, particularly for identification of therapeutic
CC   targets, and as research reagents (for RNA, in the same way that
CC   restriction endonucleases are used with DNA). The combination of
CC   modifications in (A) improves resistance to nucleases, binding affinity
CC   and/or activity. AAA23503 to AAA24747 represent oestrogen receptor
CC   hammerhead ribozyme sequences, and AAA24748 to AAA25992 represent their
CC   corresponding target sequences. AAA25993 to AAA26105 represent oestrogen
CC   receptor hairpin ribozyme sequences, and AAA26107 to AAA26218 represent
CC   their corresponding target sequences. AAA26219 to AAA26271 represent
CC   other ribozyme sequences and antisense oligonucleotides used in the
CC   exemplification of the present invention.
XX
SQ   Sequence 23 BP; 5 A; 4 C; 8 G; 3 T; 3 U; 0 other;

  Query Match             0.8%;  Score 23;  DB 21;  Length 23;
  Best Local Similarity   100.0%;  Pred. No. 6.6e+03;
  Matches   23;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy    2029 ATCAATGCTTGCACGCTGACCAC 2051
           |||||||||||||||||||||||
Db      23 ATCAATGCTTGCACGCTGACCAC 1


RESULT 15
AAA26242/c
ID   AAA26242 standard; DNA; 23 BP.
XX
AC   AAA26242;
XX
DT   19-JUL-2000  (first entry)
XX
DE   C-raf antisense oligonucleotide sequence SEQ ID NO:2740.
XX
KW   Oestrogen receptor; c-raf; k-ras; bcl-2; ribozyme; cleavage;
KW   hammerhead ribozyme; hairpin ribozyme; antisense oligonucleotide;
KW   gene expression modification; cancer; phosphorothioate; endonuclease;
KW   anticancer; breast cancer; endometrium cancer; ss.
XX
OS   Homo sapiens.
XX
PN   WO9954459-A2.
XX
PD   28-OCT-1999.
XX
PF   19-APR-1999;   99WO-US08547.
XX
PR   20-APR-1998;   98US-0082404.
PR   23-JUN-1998;   98US-0103636.
XX
PA   (RIBO-) RIBOZYME PHARM INC.
XX
PI   Thompson JD,  Beigelman L,  McSwiggen JA,  Karpeisky A,  Bellon L;
PI   Reynolds M,  Zwick M,  Jarvis T,  Woolf T,  Haeberli P;
PI   Matulic-Adamic J;
XX
DR   WPI; 2000-013248/01.
XX
PT   New nucleic acids that interact, and optionally cleave, target
PT   sequences, used to treat cancer -
```

XX
PS Example 8; Page 105; 148pp; English.
XX
CC The present invention describes nucleic acids (A) that interact stably
CC with a target sequence and contain at least one phosphoro(di)thioate
CC link, having endonuclease activity. (A), and more generally any
CC catalytic nucleic acid (A') that modulates expression of the oestrogen
CC receptor gene, are used to treat cancer (particularly of breast or
CC endometrium), in vivo or by transforming cells ex vivo and implanting
CC treated cells, or for other conditions associated with levels of
CC oestrogen receptor. Because of the high selectivity for targeted RNA, (A)
CC can also be used to correlate inhibition of gene expression with
CC alterations in phenotype, particularly for identification of therapeutic
CC targets, and as research reagents (for RNA, in the same way that
CC restriction endonucleases are used with DNA). The combination of
CC modifications in (A) improves resistance to nucleases, binding affinity
CC and/or activity. AAA23503 to AAA24747 represent oestrogen receptor
CC hammerhead ribozyme sequences, and AAA24748 to AAA25992 represent their
CC corresponding target sequences. AAA25993 to AAA26105 represent oestrogen
CC receptor hairpin ribozyme sequences, and AAA26107 to AAA26218 represent
CC their corresponding target sequences. AAA26219 to AAA26271 represent
CC other ribozyme sequences and antisense oligonucleotides used in the
CC exemplification of the present invention.
XX
SQ Sequence 23 BP; 4 A; 8 C; 5 G; 2 T; 4 U; 0 other;

Query Match 0.8%; Score 23; DB 21; Length 23;
Best Local Similarity 100.0%; Pred. No. 6.6e+03;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2483 GAATGCATGTCACAGGCGGGACT 2505
||||||||||||||||||||||
Db 23 GAATGCATGTCACAGGCGGGACT 1

Search completed: May 16, 2003, 07:08:58
Job time : 644 secs

GenCore version 5.1.4_p5_4578

OM nucleic - nucleic search, using sw model

Run on: May 16, 2003, 06:58:12 ; Search time 106 Seconds
(without alignments)
8612.988 Million cell updates/sec

Title: US-10-057-550A-64
Perfect score: 2977
Sequence: 1 ccgaatgtgaccgcctcccg.....taataaaataaattaaattt 2977

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 441362 seqs, 153338381 residues

Total number of hits satisfying chosen parameters: 609818

Minimum DB seq length: 0
Maximum DB seq length: 50

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_NA:*
1: /cgn2_6/ptodata/1/ina/5A_COMB.seq:*
2: /cgn2_6/ptodata/1/ina/5B_COMB.seq:*
3: /cgn2_6/ptodata/1/ina/6A_COMB.seq:*
4: /cgn2_6/ptodata/1/ina/6B_COMB.seq:*
5: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
6: /cgn2_6/ptodata/1/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	35.6	1.2	42	3	US-08-785-247-13	Sequence 13, Appl
	2	32.6	1.1	39	3	US-08-785-247-31	Sequence 31, Appl
	3	32.4	1.1	42	3	US-08-785-247-14	Sequence 14, Appl
	4	28	0.9	28	2	US-08-859-998-979	Sequence 979, App
	5	28	0.9	28	4	US-09-225-928-979	Sequence 979, App
c	6	26	0.9	26	1	US-08-306-691B-5	Sequence 5, Appli
	7	26	0.9	26	1	US-08-306-691B-6	Sequence 6, Appli
c	8	26	0.9	26	2	US-08-859-998-980	Sequence 980, App
c	9	26	0.9	26	4	US-09-225-928-980	Sequence 980, App
c	10	25	0.8	25	3	US-08-957-327-2	Sequence 2, Appli
c	11	25	0.8	25	4	US-09-482-084-2	Sequence 2, Appli
	12	22	0.7	43	2	US-08-850-049-17	Sequence 17, Appl
	13	22	0.7	43	2	US-08-050-478-17	Sequence 17, Appl
	14	22	0.7	43	4	US-07-858-747B-17	Sequence 17, Appl
	15	22	0.7	43	4	US-09-414-117-17	Sequence 17, Appl
	16	22	0.7	43	4	US-09-678-437-17	Sequence 17, Appl
	17	21.4	0.7	40	3	US-08-874-825-9	Sequence 9, Appli
	18	21.4	0.7	40	3	US-08-874-825-25	Sequence 25, Appl
	19	21.4	0.7	40	3	US-08-663-824-9	Sequence 9, Appli
	20	21.4	0.7	40	3	US-08-663-824-25	Sequence 25, Appl
	21	21.4	0.7	40	4	US-09-231-303-9	Sequence 9, Appli
	22	21.4	0.7	40	4	US-09-231-303-25	Sequence 25, Appl
c	23	21	0.7	40	3	US-08-874-825-10	Sequence 10, Appl
c	24	21	0.7	40	3	US-08-874-825-26	Sequence 26, Appl
c	25	21	0.7	40	3	US-08-663-824-10	Sequence 10, Appl
c	26	21	0.7	40	3	US-08-663-824-26	Sequence 26, Appl
c	27	21	0.7	40	4	US-09-231-303-10	Sequence 10, Appl
c	28	21	0.7	40	4	US-09-231-303-26	Sequence 26, Appl
	29	21	0.7	48	4	US-09-711-889-3	Sequence 3, Appli
c	30	20.4	0.7	30	4	US-09-163-507-6	Sequence 6, Appli
c	31	20.4	0.7	33	2	US-08-580-988A-11	Sequence 11, Appl
c	32	20.2	0.7	47	3	US-08-951-923-41	Sequence 41, Appl
c	33	20.2	0.7	48	1	US-08-444-734A-11	Sequence 11, Appl
c	34	20	0.7	20	1	US-08-250-856A-2	Sequence 2, Appli
c	35	20	0.7	20	1	US-08-250-856A-3	Sequence 3, Appli
c	36	20	0.7	20	1	US-08-250-856A-4	Sequence 4, Appli
c	37	20	0.7	20	1	US-08-250-856A-5	Sequence 5, Appli
c	38	20	0.7	20	1	US-08-250-856A-6	Sequence 6, Appli
c	39	20	0.7	20	1	US-08-250-856A-7	Sequence 7, Appli
c	40	20	0.7	20	1	US-08-250-856A-8	Sequence 8, Appli
c	41	20	0.7	20	1	US-08-250-856A-9	Sequence 9, Appli
c	42	20	0.7	20	1	US-08-250-856A-10	Sequence 10, Appl
c	43	20	0.7	20	1	US-08-250-856A-12	Sequence 12, Appl
c	44	20	0.7	20	1	US-08-250-856A-13	Sequence 13, Appl
c	45	20	0.7	20	1	US-08-250-856A-14	Sequence 14, Appl

ALIGNMENTS

RESULT 1
US-08-785-247-13
; Sequence 13, Application US/08785247
; Patent No. 6040149
; GENERAL INFORMATION:
; APPLICANT: Kolesnick, Richard N.
; APPLICANT: Liu, Jun
; APPLICANT: Zhang, Yuhua
; TITLE OF INVENTION: ASSAY FOR IDENTIFYING AGENTS WHICH ACT ON THE
; TITLE OF INVENTION: CERAMIDE-ACTIVATED PROTEIN KINASE, KINASE
; TITLE OF INVENTION: SUPPRESSOR OF RAS, AND METHODS OF USING SAID AGENTS
; NUMBER OF SEQUENCES: 31
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cooper & Dunham LLP
; STREET: 1185 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/785,247
; FILING DATE:
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: White, John P.
; REGISTRATION NUMBER: 28,678
; REFERENCE/DOCKET NUMBER: 48582-A/JPW/CCA
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-278-0400
; TELEFAX: 212-381-0526
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 42 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
US-08-785-247-13

Query Match 1.2%; Score 35.6; DB 3; Length 42;
Best Local Similarity 90.5%; Pred. No. 0.099;
Matches 38; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 916 GTCCACATGGTCAGCACCACGCTGCCTGTGGACAGCAGGATG 957
|||||||||||||||| |||||| || ||||||||||||||||

```
Db      1 GTCCACATGGTCAGCGTCACGCTACCGGTGGACAGCAGGATG 42


RESULT 2
US-08-785-247-31
; Sequence 31, Application US/08785247
; Patent No. 6040149
;  GENERAL INFORMATION:
;    APPLICANT:  Kolesnick, Richard N.
;    APPLICANT:  Liu, Jun
;    APPLICANT:  Zhang, Yuhua
;    TITLE OF INVENTION:  ASSAY FOR IDENTIFYING AGENTS WHICH ACT ON THE
;    TITLE OF INVENTION:  CERAMIDE-ACTIVATED PROTEIN KINASE, KINASE
;    TITLE OF INVENTION:  SUPPRESSOR OF RAS, AND METHODS OF USING SAID AGENTS
;    NUMBER OF SEQUENCES:  31
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Cooper & Dunham LLP
;      STREET:  1185 Avenue of the Americas
;      CITY:  New York
;      STATE:  New York
;      COUNTRY:  U.S.A.
;      ZIP:  10036
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/785,247
;      FILING DATE:
;      CLASSIFICATION:  514
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  White, John P.
;      REGISTRATION NUMBER:  28,678
;      REFERENCE/DOCKET NUMBER:  48582-A/JPW/CCA
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  212-278-0400
;      TELEFAX:  212-381-0526
;  INFORMATION FOR SEQ ID NO:  31:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  39 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA
US-08-785-247-31

  Query Match             1.1%;  Score 32.6;  DB 3;  Length 39;
  Best Local Similarity   89.7%;  Pred. No. 0.83;
  Matches   35;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy     919 CACATGGTCAGCACCACGCTGCCTGTGGACAGCAGGATG 957
           ||||||||||||||| ||| || |||||||||||||||
Db       1 CACATGGTCAGCACCGTGCTACCGGTGGACAGCAGGATG 39


RESULT 3
US-08-785-247-14
; Sequence 14, Application US/08785247
; Patent No. 6040149
;  GENERAL INFORMATION:
;    APPLICANT:  Kolesnick, Richard N.
;    APPLICANT:  Liu, Jun
;    APPLICANT:  Zhang, Yuhua
;    TITLE OF INVENTION:  ASSAY FOR IDENTIFYING AGENTS WHICH ACT ON THE
;    TITLE OF INVENTION:  CERAMIDE-ACTIVATED PROTEIN KINASE, KINASE
;    TITLE OF INVENTION:  SUPPRESSOR OF RAS, AND METHODS OF USING SAID AGENTS
;    NUMBER OF SEQUENCES:  31
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Cooper & Dunham LLP
;      STREET:  1185 Avenue of the Americas
;      CITY:  New York
;      STATE:  New York
;      COUNTRY:  U.S.A.
;      ZIP:  10036
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/785,247
;      FILING DATE:
;      CLASSIFICATION:  514
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  White, John P.
;      REGISTRATION NUMBER:  28,678
;      REFERENCE/DOCKET NUMBER:  48582-A/JPW/CCA
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  212-278-0400
;      TELEFAX:  212-381-0526
;  INFORMATION FOR SEQ ID NO:  14:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  42 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA
US-08-785-247-14

  Query Match             1.1%;  Score 32.4;  DB 3;  Length 42;
  Best Local Similarity   85.7%;  Pred. No. 1;
  Matches   36;  Conservative    0;  Mismatches    6;  Indels    0;  Gaps    0;

Qy     916 GTCCACATGGTCAGCACCACGCTGCCTGTGGACAGCAGGATG 957
           |||||||||||||||  |  ||| || ||||||||||||||||
Db       1 GTCCACATGGTCAGCGTCGTGCTACCGGTGGACAGCAGGATG 42


RESULT 4
US-08-859-998-979
; Sequence 979, Application US/08859998
; Patent No. 5994076
;  GENERAL INFORMATION:
;    APPLICANT:  Chenchik, Alex
;    APPLICANT:  Jokhadze, George
;    APPLICANT:  Bibilashvilli, Robert
;    TITLE OF INVENTION:  METHOD OF ASSAYING DIFFERENTIAL
;    TITLE OF INVENTION:  EXPRESSION
;    NUMBER OF SEQUENCES:  1375
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Fish & Richardson, P.C.
;      STREET:  2200 Sand Hill Road, Suite 100
;      CITY:  Menlo Park
;      STATE:  CA
;      COUNTRY:  US
;      ZIP:  94025
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  Windows95
;      SOFTWARE:  FastSEQ for Windows Version 2.0
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/859,998
;      FILING DATE:  21-MAY-1997
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Field, Bret E.
;      REGISTRATION NUMBER:  37,620
;      REFERENCE/DOCKET NUMBER:  09096/002001
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  415-322-5070
;      TELEFAX:  415-854-0875
```

```
;  INFORMATION FOR SEQ ID NO:  979:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  28 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA
;    FEATURE:
;      OTHER INFORMATION:  oligonucleotide primer
US-08-859-998-979

  Query Match             0.9%;  Score 28;  DB 2;  Length 28;
  Best Local Similarity   100.0%;  Pred. No. 18;
  Matches   28;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy   1704 CAGTTTCCAGTCGGATGTCTACTCCTAT 1731
          ||||||||||||||||||||||||||||
Db      1 CAGTTTCCAGTCGGATGTCTACTCCTAT 28


RESULT 5
US-09-225-928-979
; Sequence 979, Application US/09225928
; Patent No. 6352829
;   GENERAL INFORMATION:
;        APPLICANT: Chenchik, Alex
;                   Jokhadze, George
;                   Bibilashvilli, Robert
;        TITLE OF INVENTION: METHOD OF ASSAYING DIFFERENTIAL
;                            EXPRESSION
;        NUMBER OF SEQUENCES: 1375
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Fish & Richardson, P.C.
;             STREET: 2200 Sand Hill Road, Suite 100
;             CITY: Menlo Park
;             STATE: CA
;             COUNTRY: US
;             ZIP: 94025
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Diskette
;             COMPUTER: IBM Compatible
;             OPERATING SYSTEM: Windows95
;             SOFTWARE: FastSEQ for Windows Version 2.0
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/09/225,928
;             FILING DATE: 05-Jan-1999
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: 08/859,998
;             FILING DATE: 21-MAY-1997
;        ATTORNEY/AGENT INFORMATION:
;             NAME: Field, Bret E.
;             REGISTRATION NUMBER: 37,620
;             REFERENCE/DOCKET NUMBER: 09096/002001
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: 415-322-5070
;             TELEFAX: 415-854-0875
;   INFORMATION FOR SEQ ID NO: 979:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 28 base pairs
;             TYPE: nucleic acid
;             STRANDEDNESS: single
;             TOPOLOGY: linear
;        MOLECULE TYPE: DNA
;        FEATURE:
;             OTHER INFORMATION: oligonucleotide primer
;        SEQUENCE DESCRIPTION: SEQ ID NO: 979:
US-09-225-928-979

  Query Match             0.9%;  Score 28;  DB 4;  Length 28;
  Best Local Similarity   100.0%;  Pred. No. 18;
  Matches   28;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy   1704 CAGTTTCCAGTCGGATGTCTACTCCTAT 1731
          ||||||||||||||||||||||||||||
Db      1 CAGTTTCCAGTCGGATGTCTACTCCTAT 28


RESULT 6
US-08-306-691B-5/c
; Sequence 5, Application US/08306691B
; Patent No. 5734039
;  GENERAL INFORMATION:
;    APPLICANT:  Calabretta, Bruno
;    APPLICANT:  Skorski, Tomasz
;    TITLE OF INVENTION:  ANTISENSE
;    TITLE OF INVENTION:  OLIGONUCLEOTIDES TARGETING COOPERATING ONCOGENES
;    NUMBER OF SEQUENCES:  55
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Seidel, Gonda, Lavorgna & Monaco, P.C.
;      STREET:  Two Penn Center, Suite 1800
;      CITY:  Philadelphia
;      STATE:  Pennsylvania
;      COUNTRY:  U.S.A.
;      ZIP:  19102
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette, 3.50 inch, 720 Kb
;      COMPUTER:  IBM PS/2
;      OPERATING SYSTEM:  MS-DOS
;      SOFTWARE:  WordPerfect 5.1
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/306,691B
;      FILING DATE:  September 15, 1994
;      CLASSIFICATION:  514
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Monaco, Daniel A.
;      REGISTRATION NUMBER:  30,480
;      REFERENCE/DOCKET NUMBER:  8321-8
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (215) 568-8383
;      TELEFAX:  (215) 568-5549
;      TELEX:  No. 5734039e
;  INFORMATION FOR SEQ ID NO:  5:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  26 Nucleotides
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single stranded
;      TOPOLOGY:  linear
US-08-306-691B-5

  Query Match             0.9%;  Score 26;  DB 1;  Length 26;
  Best Local Similarity   100.0%;  Pred. No. 75;
  Matches   26;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       5 ATGTGACCGCCTCCCGCTCCCTCACC 30
           ||||||||||||||||||||||||||
Db      26 ATGTGACCGCCTCCCGCTCCCTCACC 1


RESULT 7
US-08-306-691B-6
; Sequence 6, Application US/08306691B
; Patent No. 5734039
;  GENERAL INFORMATION:
;    APPLICANT:  Calabretta, Bruno
;    APPLICANT:  Skorski, Tomasz
;    TITLE OF INVENTION:  ANTISENSE
;    TITLE OF INVENTION:  OLIGONUCLEOTIDES TARGETING COOPERATING ONCOGENES
;    NUMBER OF SEQUENCES:  55
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Seidel, Gonda, Lavorgna & Monaco, P.C.
;      STREET:  Two Penn Center, Suite 1800
;      CITY:  Philadelphia
```

```
;       STATE:  Pennsylvania
;       COUNTRY:  U.S.A.
;       ZIP:  19102
;     COMPUTER READABLE FORM:
;       MEDIUM TYPE:  Diskette, 3.50 inch, 720 Kb
;       COMPUTER:  IBM PS/2
;       OPERATING SYSTEM:  MS-DOS
;       SOFTWARE:  WordPerfect 5.1
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  US/08/306,691B
;       FILING DATE:  September 15, 1994
;       CLASSIFICATION:  514
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:
;       FILING DATE:
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  Monaco, Daniel A.
;       REGISTRATION NUMBER:  30,480
;       REFERENCE/DOCKET NUMBER:  8321-8
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  (215) 568-8383
;       TELEFAX:  (215) 568-5549
;       TELEX:  No. 5734039e
;   INFORMATION FOR SEQ ID NO:  6:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  26 Nucleotides
;       TYPE:  nucleic acid
;       STRANDEDNESS:  single stranded
;       TOPOLOGY:  linear
US-08-306-691B-6

  Query Match             0.9%;  Score 26;  DB 1;  Length 26;
  Best Local Similarity   100.0%;  Pred. No. 75;
  Matches   26;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       5 ATGTGACCGCCTCCCGCTCCCTCACC 30
           ||||||||||||||||||||||||||
Db       1 ATGTGACCGCCTCCCGCTCCCTCACC 26


RESULT 8
US-08-859-998-980/c
; Sequence 980, Application US/08859998
; Patent No. 5994076
;  GENERAL INFORMATION:
;     APPLICANT:  Chenchik, Alex
;     APPLICANT:  Jokhadze, George
;     APPLICANT:  Bibilashvilli, Robert
;     TITLE OF INVENTION:  METHOD OF ASSAYING DIFFERENTIAL
;     TITLE OF INVENTION:  EXPRESSION
;     NUMBER OF SEQUENCES:  1375
;     CORRESPONDENCE ADDRESS:
;       ADDRESSEE:  Fish & Richardson, P.C.
;       STREET:  2200 Sand Hill Road, Suite 100
;       CITY:  Menlo Park
;       STATE:  CA
;       COUNTRY:  US
;       ZIP:  94025
;     COMPUTER READABLE FORM:
;       MEDIUM TYPE:  Diskette
;       COMPUTER:  IBM Compatible
;       OPERATING SYSTEM:  Windows95
;       SOFTWARE:  FastSEQ for Windows Version 2.0
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  US/08/859,998
;       FILING DATE:  21-MAY-1997
;       CLASSIFICATION:  435
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:
;       FILING DATE:
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  Field, Bret E.
;       REGISTRATION NUMBER:  37,620
;       REFERENCE/DOCKET NUMBER:  09096/002001
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  415-322-5070
;       TELEFAX:  415-854-0875
;   INFORMATION FOR SEQ ID NO:  980:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  26 base pairs
;       TYPE:  nucleic acid
;       STRANDEDNESS:  single
;       TOPOLOGY:  linear
;     MOLECULE TYPE:  DNA
;     FEATURE:
;       OTHER INFORMATION:  oligonucleotide primer
US-08-859-998-980

  Query Match             0.9%;  Score 26;  DB 2;  Length 26;
  Best Local Similarity   100.0%;  Pred. No. 75;
  Matches   26;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy    1963 TCTCTACCGAAGATCAACCGGAGCGC 1988
           ||||||||||||||||||||||||||
Db      26 TCTCTACCGAAGATCAACCGGAGCGC 1


RESULT 9
US-09-225-928-980/c
; Sequence 980, Application US/09225928
; Patent No. 6352829
;  GENERAL INFORMATION:
;       APPLICANT: Chenchik, Alex
;                  Jokhadze, George
;                  Bibilashvilli, Robert
;       TITLE OF INVENTION: METHOD OF ASSAYING DIFFERENTIAL
;                           EXPRESSION
;       NUMBER OF SEQUENCES: 1375
;       CORRESPONDENCE ADDRESS:
;            ADDRESSEE: Fish & Richardson, P.C.
;            STREET: 2200 Sand Hill Road, Suite 100
;            CITY: Menlo Park
;            STATE: CA
;            COUNTRY: US
;            ZIP: 94025
;       COMPUTER READABLE FORM:
;            MEDIUM TYPE: Diskette
;            COMPUTER: IBM Compatible
;            OPERATING SYSTEM: Windows95
;            SOFTWARE: FastSEQ for Windows Version 2.0
;       CURRENT APPLICATION DATA:
;            APPLICATION NUMBER: US/09/225,928
;            FILING DATE: 05-Jan-1999
;            CLASSIFICATION: <Unknown>
;       PRIOR APPLICATION DATA:
;            APPLICATION NUMBER: 08/859,998
;            FILING DATE: 21-MAY-1997
;       ATTORNEY/AGENT INFORMATION:
;            NAME: Field, Bret E.
;            REGISTRATION NUMBER: 37,620
;            REFERENCE/DOCKET NUMBER: 09096/002001
;       TELECOMMUNICATION INFORMATION:
;            TELEPHONE: 415-322-5070
;            TELEFAX: 415-854-0875
;   INFORMATION FOR SEQ ID NO: 980:
;       SEQUENCE CHARACTERISTICS:
;            LENGTH: 26 base pairs
;            TYPE: nucleic acid
;            STRANDEDNESS: single
;            TOPOLOGY: linear
;       MOLECULE TYPE: DNA
;       FEATURE:
;            OTHER INFORMATION:  oligonucleotide primer
;       SEQUENCE DESCRIPTION: SEQ ID NO: 980:
US-09-225-928-980
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Qy   1963 TCTCTACCGAAGATCAACCGGAGCGC 1988
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Db     26 TCTCTACCGAAGATCAACCGGAGCGC 1


RESULT 10
US-08-957-327-2/c
; Sequence 2, Application US/08957327
; Patent No. 6126965
;  GENERAL INFORMATION:
;    APPLICANT:  Kasid, Usha
;    APPLICANT:  Gokhale, Prafulla
;    APPLICANT:  Dritschilo, Anatoly
;    APPLICANT:  Rahman, Aqulur
;    TITLE OF INVENTION:  Liposomes contaiing Oligonucelotides
;    NUMBER OF SEQUENCES:  3
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Hendricks and Assoc.
;      STREET:  P.O. Box 2509
;      CITY:  Fairfax
;      STATE:  VA
;      COUNTRY:  US
;      ZIP:  22031
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/957,327
;      FILING DATE:  24-OCT-1997
;      CLASSIFICATION:  514
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Hendricks, Glenna
;      REGISTRATION NUMBER:  32,535
;      REFERENCE/DOCKET NUMBER:  kasid
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (703) 591-4470
;      TELEFAX:  (703) 591-4428
;  INFORMATION FOR SEQ ID NO:  2:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  25 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  unknown
;    MOLECULE TYPE:  DNA (genomic)
;    HYPOTHETICAL:  NO
;    ANTI-SENSE:  YES
US-08-957-327-2

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  Matches   25;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy    121 GCTGCATCAATGGAGCACATACAGG 145
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Db     25 GCTGCATCAATGGAGCACATACAGG 1


RESULT 11
US-09-482-084-2/c
; Sequence 2, Application US/09482084
; Patent No. 6333314
;  GENERAL INFORMATION:
;       APPLICANT: Kasid, Usha
;                  Gokhale, Prafulla
;                  Dritschilo, Anatoly
;                  Rahman, Aqulur
;       TITLE OF INVENTION: Liposomes contaiing Oligonucelotides
;       NUMBER OF SEQUENCES: 3
;       CORRESPONDENCE ADDRESS:
;            ADDRESSEE: Hendricks and Assoc.
;            STREET: P.O. Box 2509
;            CITY: Fairfax
;            STATE: VA
;            COUNTRY: US
;            ZIP: 22031
;       COMPUTER READABLE FORM:
;            MEDIUM TYPE: Floppy disk
;            COMPUTER: IBM PC compatible
;            OPERATING SYSTEM: PC-DOS/MS-DOS
;            SOFTWARE: PatentIn Release #1.0, Version #1.25
;       CURRENT APPLICATION DATA:
;            APPLICATION NUMBER: US/09/482,084
;            FILING DATE: 13-Jan-2000
;            CLASSIFICATION: <Unknown>
;       PRIOR APPLICATION DATA:
;            APPLICATION NUMBER: 08/957,327
;            FILING DATE: <Unknown>
;       ATTORNEY/AGENT INFORMATION:
;            NAME: Hendricks, Glenna
;            REGISTRATION NUMBER: 32,535
;            REFERENCE/DOCKET NUMBER: kasid
;       TELECOMMUNICATION INFORMATION:
;            TELEPHONE: (703) 591-4470
;            TELEFAX: (703) 591-4428
;   INFORMATION FOR SEQ ID NO: 2:
;       SEQUENCE CHARACTERISTICS:
;            LENGTH: 25 base pairs
;            TYPE: nucleic acid
;            STRANDEDNESS: single
;            TOPOLOGY: unknown
;       MOLECULE TYPE: DNA (genomic)
;       HYPOTHETICAL: NO
;       ANTI-SENSE: YES
;       SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-482-084-2

  Query Match             0.8%;  Score 25;  DB 4;  Length 25;
  Best Local Similarity   100.0%;  Pred. No. 1.5e+02;
  Matches   25;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy    121 GCTGCATCAATGGAGCACATACAGG 145
          |||||||||||||||||||||||||
Db     25 GCTGCATCAATGGAGCACATACAGG 1


RESULT 12
US-08-850-049-17
; Sequence 17, Application US/08850049
; Patent No. 5965726
;  GENERAL INFORMATION:
;    APPLICANT:
;    APPLICANT:
;    APPLICANT:
;    TITLE OF INVENTION:  METHOD OF ELIMINATING
;    TITLE OF INVENTION:  INHIBITORY/INSTABILITY REGIONS OF mRNA
;    NUMBER OF SEQUENCES:  130
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  MORGAN & FINNEGAN
;      STREET:  345 PARK AVENUE
;      CITY:  NEW YORK
;      STATE:  NEW YORK
;      COUNTRY:  USA
;      ZIP:  10154
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  FLOPPY DISK
;      COMPUTER:  IBM PC COMPATIBLE
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  WORDPERFECT 5.1
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/850,049
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;       FILING DATE:  02-MAY-1997
;       CLASSIFICATION:  435
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  US 08/050,478
;       FILING DATE:  26-OCT-1994
;       CLASSIFICATION:  435
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  PCT/US93/02908
;       FILING DATE:  29-MAR-1993
;       CLASSIFICATION:  435
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  US 07/858,747
;       FILING DATE:  27-MAR-1992
;       CLASSIFICATION:  435
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  MORRY, MARY J.
;       REGISTRATION NUMBER:  34,398
;       REFERENCE/DOCKET NUMBER:  2026-4006US1
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  (212)758-4800
;       TELEFAX:  (212)751-6849
;   INFORMATION FOR SEQ ID NO:  17:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  43 BASE PAIRS
;       TYPE:  NUCLEIC ACID
;       STRANDEDNESS:  SINGLE
;       TOPOLOGY:  LINEAR
US-08-850-049-17

  Query Match             0.7%;  Score 22;  DB 2;  Length 43;
  Best Local Similarity   73.7%;  Pred. No. 1.9e+03;
  Matches   28;  Conservative    0;  Mismatches   10;  Indels    0;  Gaps    0;

Qy    2207 TCACAGGGCCTTAACTTCATGTTGCCTTCTTTTCTATC 2244
           || |||   | || |||||| ||||||| || |||| |
Db       2 TCTCAGATACCTAGCTTCATATTGCCTTATTGTCTACC 39


RESULT 13
US-08-050-478-17
; Sequence 17, Application US/08050478
; Patent No. 5972596
;  GENERAL INFORMATION:
;    APPLICANT:
;    APPLICANT:
;    APPLICANT:
;    TITLE OF INVENTION:  METHOD OF ELIMINATING
;    TITLE OF INVENTION:  INHIBITORY/INSTABILITY REGIONS OF mRNA
;    NUMBER OF SEQUENCES:  130
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  MORGAN & FINNEGAN
;      STREET:  345 PARK AVENUE
;      CITY:  NEW YORK
;      STATE:  NEW YORK
;      COUNTRY:  USA
;      ZIP:  10154
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  FLOPPY DISK
;      COMPUTER:  IBM PC COMPATIBLE
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  WORDPERFECT 5.1
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/050,478
;      FILING DATE:  26-OCT-1994
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/US93/02908
;      FILING DATE:  29-MAR-1993
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/858,747
;      FILING DATE:  27-MAR-1992
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  MORRY, MARY J.
;      REGISTRATION NUMBER:  34,398
;      REFERENCE/DOCKET NUMBER:  2026-4006US1
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (212)758-4800
;      TELEFAX:  (212)751-6849
;  INFORMATION FOR SEQ ID NO:  17:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  43 BASE PAIRS
;      TYPE:  NUCLEIC ACID
;      STRANDEDNESS:  SINGLE
;      TOPOLOGY:  LINEAR
US-08-050-478-17

  Query Match             0.7%;  Score 22;  DB 2;  Length 43;
  Best Local Similarity   73.7%;  Pred. No. 1.9e+03;
  Matches   28;  Conservative    0;  Mismatches   10;  Indels    0;  Gaps    0;

Qy    2207 TCACAGGGCCTTAACTTCATGTTGCCTTCTTTTCTATC 2244
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Db       2 TCTCAGATACCTAGCTTCATATTGCCTTATTGTCTACC 39


RESULT 14
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; Sequence 17, Application US/07858747B
; Patent No. 6174666
;  GENERAL INFORMATION:
;    APPLICANT:  PAVLAKIS, GEORGE N.; FELBER, BARBARA
;    APPLICANT:  K.
;    TITLE OF INVENTION:  METHOD OF ELIMINATING
;    TITLE OF INVENTION:  INHIBITORY/INSTABILITY REGIONS OF mRNA
;    NUMBER OF SEQUENCES:  21
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  MORGAN & FINNEGAN
;      STREET:  345 PARK AVENUE
;      CITY:  NEW YORK
;      STATE:  NEW YORK
;      COUNTRY:  USA
;      ZIP:  10154
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  FLOPPY DISK
;      COMPUTER:  IBM PC COMPATIBLE
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  WORDPERFECT 5.1
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/07/858,747B
;      FILING DATE:  19920327
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  MARY J. MORRY
;      REGISTRATION NUMBER:  34,398
;      REFERENCE/DOCKET NUMBER:  2026-4006
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (212)758-4800
;      TELEFAX:  (212)751-6849
;  INFORMATION FOR SEQ ID NO:  17:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  43
;      TYPE:  NUCLEIC ACID
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;      TOPOLOGY:  UNKNOWN
;    MOLECULE TYPE:  OTHER
;    HYPOTHETICAL:  YES
;    FEATURE:
;      NAME/KEY:
;      LOCATION:
;      IDENTIFICATION METHOD:
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US-07-858-747B-17

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  Matches   28;  Conservative    0;  Mismatches   10;  Indels    0;  Gaps    0;

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Db       2 TCTCAGATACCTAGCTTCATATTGCCTTATTGTCTACC 39


RESULT 15
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; Sequence 17, Application US/09414117
; Patent No. 6291664
;  GENERAL INFORMATION:
;    APPLICANT:
;    APPLICANT:
;    APPLICANT:
;    TITLE OF INVENTION:  METHOD OF ELIMINATING
;    TITLE OF INVENTION:  INHIBITORY/INSTABILITY REGIONS OF mRNA
;    NUMBER OF SEQUENCES:  130
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  MORGAN & FINNEGAN
;      STREET:  345 PARK AVENUE
;      CITY:  NEW YORK
;      STATE:  NEW YORK
;      COUNTRY:  USA
;      ZIP:  10154
;    COMPUTER READABLE FORM:
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;      COMPUTER:  IBM PC COMPATIBLE
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
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;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/414,117
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/850,049
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/US93/02908
;      FILING DATE:  29-MAR-1993
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/858,747
;      FILING DATE:  27-MAR-1992
;      CLASSIFICATION:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  MORRY, MARY J.
;      REGISTRATION NUMBER:  34,398
;      REFERENCE/DOCKET NUMBER:  2026-4006US1
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (212)758-4800
;      TELEFAX:  (212)751-6849
;  INFORMATION FOR SEQ ID NO:  17:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  43 BASE PAIRS
;      TYPE:  NUCLEIC ACID
;      STRANDEDNESS:  SINGLE
;      TOPOLOGY:  LINEAR
US-09-414-117-17

  Query Match             0.7%;  Score 22;  DB 4;  Length 43;
  Best Local Similarity   73.7%;  Pred. No. 1.9e+03;
  Matches   28;  Conservative    0;  Mismatches   10;  Indels    0;  Gaps    0;

Qy    2207 TCACAGGGCCTTAACTTCATGTTGCCTTCTTTTCTATC 2244
           || |||   | || |||||| ||||||| || |||| |
Db       2 TCTCAGATACCTAGCTTCATATTGCCTTATTGTCTACC 39
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Search completed: May 16, 2003, 12:18:33
Job time : 113 secs

GenCore version 5.1.4_p5_4578

OM nucleic - nucleic search, using sw model

Run on: May 16, 2003, 09:19:06 ; Search time 376 Seconds
(without alignments)
10213.154 Million cell updates/sec

Title: US-10-057-550A-64
Perfect score: 2977
Sequence: 1 ccgaatgtgaccgcctcccg.....taataaaataaattaaattt 2977

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 810007 seqs, 644969091 residues

Total number of hits satisfying chosen parameters: 482682

Minimum DB seq length: 0
Maximum DB seq length: 50

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.		Score	% Query Match	Length	DB	ID	Description
1		30.6	1.0	31	10	US-09-801-274-835	Sequence 835, App
2	c	25	0.8	25	9	US-09-930-283A-2	Sequence 2, Appli
3		22	0.7	43	9	US-09-943-722-17	Sequence 17, Appl
4		20.6	0.7	21	10	US-09-765-081-213	Sequence 213, App
5	c	20.6	0.7	47	9	US-09-764-891-10177	Sequence 10177, A
6	c	20.4	0.7	31	10	US-09-263-959-580	Sequence 580, App
7		20.4	0.7	41	9	US-10-085-906-99	Sequence 99, Appl
8		20.2	0.7	46	10	US-09-827-289-19	Sequence 19, Appl
9		20.2	0.7	46	10	US-09-827-289-23	Sequence 23, Appl
10		20.2	0.7	48	10	US-09-822-698A-62	Sequence 62, Appl
11	c	20	0.7	20	9	US-10-103-906-4	Sequence 4, Appli
12		20	0.7	20	9	US-10-078-949-3	Sequence 3, Appli
13		20	0.7	20	9	US-10-078-949-5	Sequence 5, Appli
14		20	0.7	20	9	US-10-078-949-7	Sequence 7, Appli
15	c	20	0.7	20	9	US-09-835-371-37	Sequence 37, Appl
16	c	20	0.7	20	9	US-09-996-263-7	Sequence 7, Appli
17	c	20	0.7	20	9	US-09-996-263-8	Sequence 8, Appli
18	c	20	0.7	20	9	US-09-996-263-9	Sequence 9, Appli
19	c	20	0.7	20	9	US-09-996-263-10	Sequence 10, Appl
20	c	20	0.7	20	9	US-09-996-263-11	Sequence 11, Appl
21	c	20	0.7	20	9	US-09-996-263-12	Sequence 12, Appl
22	c	20	0.7	20	9	US-09-996-263-13	Sequence 13, Appl
23	c	20	0.7	20	9	US-09-996-263-14	Sequence 14, Appl
24	c	20	0.7	20	9	US-09-835-370-37	Sequence 37, Appl
25	c	20	0.7	20	9	US-10-071-822A-1	Sequence 1, Appli
26	c	20	0.7	20	9	US-09-932-300-76	Sequence 76, Appl
27	c	20	0.7	20	9	US-10-057-550-2	Sequence 2, Appli
28	c	20	0.7	20	9	US-10-057-550-3	Sequence 3, Appli
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32	c	20	0.7	20	9	US-10-057-550-7	Sequence 7, Appli
33	c	20	0.7	20	9	US-10-057-550-8	Sequence 8, Appli
34	c	20	0.7	20	9	US-10-057-550-9	Sequence 9, Appli
35	c	20	0.7	20	9	US-10-057-550-10	Sequence 10, Appl
36	c	20	0.7	20	9	US-10-057-550-12	Sequence 12, Appl
37	c	20	0.7	20	9	US-10-057-550-13	Sequence 13, Appl
38	c	20	0.7	20	9	US-10-057-550-14	Sequence 14, Appl
39	c	20	0.7	20	9	US-10-057-550-15	Sequence 15, Appl
40	c	20	0.7	20	9	US-10-057-550-16	Sequence 16, Appl
41	c	20	0.7	20	9	US-10-057-550-17	Sequence 17, Appl
42	c	20	0.7	20	9	US-10-057-550-18	Sequence 18, Appl
43	c	20	0.7	20	9	US-10-057-550-19	Sequence 19, Appl
44	c	20	0.7	20	9	US-10-057-550-20	Sequence 20, Appl
45	c	20	0.7	20	9	US-10-057-550-21	Sequence 21, Appl

ALIGNMENTS

RESULT 1
US-09-801-274-835
; Sequence 835, Application US/09801274
; Patent No. US20020032319A1
; GENERAL INFORMATION:
; APPLICANT: Cargill, Michele
; APPLICANT: Ireland, James S.
; APPLICANT: Lander, Eric S.
; TITLE OF INVENTION: HUMAN SINGLE NUCLEOTIDE POLYMORPHISMS
; FILE REFERENCE: 2825.2009-001
; CURRENT APPLICATION NUMBER: US/09/801,274
; CURRENT FILING DATE: 2001-03-07
; PRIOR APPLICATION NUMBER: US 60/187,510
; PRIOR FILING DATE: 2000-03-07
; PRIOR APPLICATION NUMBER: US 60/206,129
; PRIOR FILING DATE: 2000-05-22
; NUMBER OF SEQ ID NOS: 1802
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 835
; LENGTH: 31
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-801-274-835

Query Match 1.0%; Score 30.6; DB 10; Length 31;
Best Local Similarity 96.8%; Pred. No. 13;
Matches 30; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 2144 CCCTTTCTCCAGAGGCAGAACACATGTTTTC 2174
||||||||||||||||:||||||||||||||
Db 1 CCCTTTCTCCAGAGGYAGAACACATGTTTTC 31

RESULT 2
US-09-930-283A-2/c
; Sequence 2, Application US/09930283A
; Patent No. US20020160038A1
; GENERAL INFORMATION:
; APPLICANT: Kasid, Usha
; Gokhale, Prafulla
; Dritschilo, Anatoly
; Rahman, Aqulur

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;       TITLE OF INVENTION: Liposomes contaiing Oligonucelotides
;       NUMBER OF SEQUENCES: 3
;       CORRESPONDENCE ADDRESS:
;            ADDRESSEE: Hendricks and Assoc.
;            STREET: P.O. Box 2509
;            CITY: Fairfax
;            STATE: VA
;            COUNTRY: US
;            ZIP: 22031
;       COMPUTER READABLE FORM:
;            MEDIUM TYPE: Floppy disk
;            COMPUTER: IBM PC compatible
;            OPERATING SYSTEM: PC-DOS/MS-DOS
;            SOFTWARE: PatentIn Release #1.0, Version #1.25
;       CURRENT APPLICATION DATA:
;            APPLICATION NUMBER: US/09/930,283A
;            FILING DATE: 16-Aug-2001
;            CLASSIFICATION: <Unknown>
;       PRIOR APPLICATION DATA:
;            APPLICATION NUMBER: 09/354,109
;            FILING DATE: 1999-07-15
;       ATTORNEY/AGENT INFORMATION:
;            NAME: Hendricks, Glenna
;            REGISTRATION NUMBER: 32,535
;            REFERENCE/DOCKET NUMBER: kasid
;       TELECOMMUNICATION INFORMATION:
;            TELEPHONE: (703) 591-4470
;            TELEFAX: (703) 591-4428
;   INFORMATION FOR SEQ ID NO: 2:
;       SEQUENCE CHARACTERISTICS:
;            LENGTH: 25 base pairs
;            TYPE: nucleic acid
;            STRANDEDNESS: single
;            TOPOLOGY: unknown
;       MOLECULE TYPE: DNA (genomic)
;       HYPOTHETICAL: NO
;       ANTI-SENSE: YES
;       SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-930-283A-2

  Query Match             0.8%;  Score 25;  DB 9;  Length 25;
  Best Local Similarity   100.0%;  Pred. No. 7.1e+02;
  Matches   25;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy     121 GCTGCATCAATGGAGCACATACAGG 145
           |||||||||||||||||||||||||
Db      25 GCTGCATCAATGGAGCACATACAGG 1


RESULT 3
US-09-943-722-17
; Sequence 17, Application US/09943722
; Publication No. US20020192660A1
;  GENERAL INFORMATION:
;    APPLICANT:
;    APPLICANT:
;    APPLICANT:
;    TITLE OF INVENTION:  METHOD OF ELIMINATING
;    TITLE OF INVENTION:  INHIBITORY/INSTABILITY REGIONS OF mRNA
;    NUMBER OF SEQUENCES:  130
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  MORGAN & FINNEGAN
;      STREET:  345 PARK AVENUE
;      CITY:  NEW YORK
;      STATE:  NEW YORK
;      COUNTRY:  USA
;      ZIP:  10154
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  FLOPPY DISK
;      COMPUTER:  IBM PC COMPATIBLE
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  WORDPERFECT 5.1
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/943,722
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/850,049
;      FILING DATE:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/050,478
;      FILING DATE:  26-OCT-1994
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/US93/02908
;      FILING DATE:  29-MAR-1993
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/858,747
;      FILING DATE:  27-MAR-1992
;      CLASSIFICATION:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  MORRY, MARY J.
;      REGISTRATION NUMBER:  34,398
;      REFERENCE/DOCKET NUMBER:  2026-4006US1
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (212)758-4800
;      TELEFAX:  (212)751-6849
;  INFORMATION FOR SEQ ID NO:  17:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  43 BASE PAIRS
;      TYPE:  NUCLEIC ACID
;      STRANDEDNESS:  SINGLE
;      TOPOLOGY:  LINEAR
US-09-943-722-17

  Query Match             0.7%;  Score 22;  DB 9;  Length 43;
  Best Local Similarity   73.7%;  Pred. No. 9.3e+03;
  Matches   28;  Conservative    0;  Mismatches   10;  Indels    0;  Gaps    0;

Qy    2207 TCACAGGGCCTTAACTTCATGTTGCCTTCTTTTCTATC 2244
           || |||   | || |||||| ||||||| || |||| |
Db       2 TCTCAGATACCTAGCTTCATATTGCCTTATTGTCTACC 39


RESULT 4
US-09-765-081-213
; Sequence 213, Application US/09765081
; Patent No. US20020037508A1
; GENERAL INFORMATION:
;  APPLICANT: Cargill, Michele
;  APPLICANT:  Ireland, James S.
;  APPLICANT:  Lander, Eric S.
;  TITLE OF INVENTION: HUMAN SINGLE NUCLEOTIDE POLYMORPHISMS
;  FILE REFERENCE: 2825.2008-001
;  CURRENT APPLICATION NUMBER: US/09/765,081
;  CURRENT FILING DATE:  2001-01-18
;  PRIOR APPLICATION NUMBER: US 60/176,861
;  PRIOR FILING DATE: 2000-01-19
;  NUMBER OF SEQ ID NOS: 461
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 213
;   LENGTH: 21
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-765-081-213

  Query Match             0.7%;  Score 20.6;  DB 10;  Length 21;
  Best Local Similarity   95.2%;  Pred. No. 1.6e+04;
  Matches   20;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy    1237 GGAGATGTTGCAGTAAAGATC 1257
           ||||||||||:||||||||||
Db       1 GGAGATGTTGSAGTAAAGATC 21
```

```
RESULT 5
US-09-764-891-10177/c
; Sequence 10177, Application US/09764891
; Publication No. US20030077808A1
; GENERAL INFORMATION:
;  APPLICANT: Rosen et al.
;  TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
;  FILE REFERENCE: PC006
;  CURRENT APPLICATION NUMBER: US/09/764,891
;  CURRENT FILING DATE:  2001-01-17
;  Prior application data removed - consult PALM or file wrapper
;  NUMBER OF SEQ ID NOS: 10231
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 10177
;   LENGTH: 47
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-764-891-10177

  Query Match             0.7%;  Score 20.6;  DB 9;  Length 47;
  Best Local Similarity   67.4%;  Pred. No. 2.8e+04;
  Matches   29;  Conservative    0;  Mismatches   14;  Indels    0;  Gaps    0;

Qy   2868 ACAGGTTTTCTTGATGATTTGGGTTTTAATTTTGTTTTTATTG 2910
           |||| |||| ||  |  |||   ||||  |||| |||||  | |
Db     47 ACAGATTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTAG 5


RESULT 6
US-09-263-959-580/c
; Sequence 580, Application US/09263959
; Patent No. US20020150891A1
;  GENERAL INFORMATION:
;    APPLICANT:  Hood, Leroy E.
;    APPLICANT:  Rowen, Lee
;    APPLICANT:  Koop, Ben F.
;    TITLE OF INVENTION:  DIAGNOSTIC AND THERAPEUTIC COMPOSITIONS AND METHODS WHICH UTI
;    NUMBER OF SEQUENCES:  1279
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Seed and Berry LLP
;      STREET:  6300 Columbia Center, 701 Fifth Avenue
;      CITY:  Seattle
;      STATE:  Washington
;      COUNTRY:  US
;      ZIP:  98104-7092
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/263,959
;      FILING DATE:  05-MAR-1999
;      CLASSIFICATION:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  McMasters, David D.
;      REGISTRATION NUMBER:  33,963
;      REFERENCE/DOCKET NUMBER:  920010.426C2
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (206) 622-4900
;      TELEFAX:  (206) 682-6031
;  INFORMATION FOR SEQ ID NO:  580:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  31 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
US-09-263-959-580

  Query Match             0.7%;  Score 20.4;  DB 10;  Length 31;
  Best Local Similarity   95.5%;  Pred. No. 2.4e+04;
  Matches   21;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy   2799 CTAACAAACAAACAAACAAACA 2820
          | ||||||||||||||||||||
Db     28 CAAACAAACAAACAAACAAACA 7


RESULT 7
US-10-085-906-99
; Sequence 99, Application US/10085906
; Publication No. US20030054371A1
; GENERAL INFORMATION:
;  APPLICANT: Ying, Vincent
;  APPLICANT:  Wu, Paul
;  APPLICANT:  Gray, Gary S.
;  TITLE OF INVENTION: POLYMORPHIC ELEMENTS IN THE
;  TITLE OF INVENTION:  COSTIMULATORY RECEPTOR LOCUS AND USES THEREOF
;  FILE REFERENCE: GNN-5343CP2
;  CURRENT APPLICATION NUMBER: US/10/085,906
;  CURRENT FILING DATE:  2002-02-27
;  PRIOR APPLICATION NUMBER: US 60/126,215
;  PRIOR FILING DATE: 1999-03-25
;  PRIOR APPLICATION NUMBER: US 09/534,061
;  PRIOR FILING DATE: 2000-03-24
;  PRIOR APPLICATION NUMBER: PCT/US00/07938
;  PRIOR FILING DATE: 2000-03-24
;  NUMBER OF SEQ ID NOS: 545
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 99
;   LENGTH: 41
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-085-906-99

  Query Match             0.7%;  Score 20.4;  DB 9;  Length 41;
  Best Local Similarity   95.5%;  Pred. No. 2.9e+04;
  Matches   21;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy   2799 CTAACAAACAAACAAACAAACA 2820
          | ||||||||||||||||||||
Db      8 CAAACAAACAAACAAACAAACA 29


RESULT 8
US-09-827-289-19
; Sequence 19, Application US/09827289
; Patent No. US20020009716A1
; GENERAL INFORMATION:
;  APPLICANT: Abarzua, Patricio
;  TITLE OF INVENTION: Process for Allele Discrimination Using Primer
;  TITLE OF INVENTION:  Extension
;  FILE REFERENCE: 469290-55
;  CURRENT APPLICATION NUMBER: US/09/827,289
;  CURRENT FILING DATE:  2001-04-05
;  PRIOR APPLICATION NUMBER: U.S. 60/194843
;  PRIOR FILING DATE: 2000-04-05
;  NUMBER OF SEQ ID NOS: 35
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 19
;   LENGTH: 46
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: P1 primer for
;   OTHER INFORMATION: use in allele discrimination
US-09-827-289-19

  Query Match             0.7%;  Score 20.2;  DB 10;  Length 46;
  Best Local Similarity   68.3%;  Pred. No. 3.7e+04;
  Matches   28;  Conservative    0;  Mismatches   13;  Indels    0;  Gaps    0;

Qy   2893 TTAATTTTGTTTTTATTGCACCTGACAAAATACAGTTATCT 2933
          ||  |||| ||||| | | |  ||||||||  || || | |
Db      1 TTTTTTTTTTTTTTTTAGAAGATGACAAAAATCATTTCTAT 41
```

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RESULT 9
US-09-827-289-23
; Sequence 23, Application US/09827289
; Patent No. US20020009716A1
; GENERAL INFORMATION:
;  APPLICANT: Abarzua, Patricio
;  TITLE OF INVENTION: Process for Allele Discrimination Using Primer
;  TITLE OF INVENTION:  Extension
;  FILE REFERENCE: 469290-55
;  CURRENT APPLICATION NUMBER: US/09/827,289
;  CURRENT FILING DATE:  2001-04-05
;  PRIOR APPLICATION NUMBER: U.S. 60/194843
;  PRIOR FILING DATE: 2000-04-05
;  NUMBER OF SEQ ID NOS: 35
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 23
;   LENGTH: 46
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: P1 primer for
;   OTHER INFORMATION: use in allele discrimination
US-09-827-289-23

  Query Match             0.7%;  Score 20.2;  DB 10;  Length 46;
  Best Local Similarity   68.3%;  Pred. No. 3.7e+04;
  Matches   28;  Conservative    0;  Mismatches   13;  Indels    0;  Gaps    0;

Qy    2893 TTAATTTTGTTTTTATTGCACCTGACAAAATACAGTTATCT 2933
           ||  |||| |||||  | | |  ||||||||  || || | |
Db       1 TTTTTTTTTTTTTTTTAGAAGATGACAAAAATCATTTCTAT 41


RESULT 10
US-09-822-698A-62
; Sequence 62, Application US/09822698A
; Patent No. US20020146750A1
; GENERAL INFORMATION:
;  APPLICANT: Hoogenboom, Hendricus R.J.M.
;  APPLICANT:  Henderikx, Maria P.G.
;  TITLE OF INVENTION: MUCIN-1 Specific Binding Members and Methods of Use Thereof
;  FILE REFERENCE: DYX-015.1 US
;  CURRENT APPLICATION NUMBER: US/09/822,698A
;  CURRENT FILING DATE:  2001-03-30
;  PRIOR APPLICATION NUMBER: US 09/538,913
;  PRIOR FILING DATE: 2000-03-30
;  NUMBER OF SEQ ID NOS: 112
;  SOFTWARE: Microsoft Word
; SEQ ID NO 62
;   LENGTH: 48
;   TYPE: DNA
;   ORGANISM: artificial sequence
;   FEATURE:
;   OTHER INFORMATION: nucleotide sequence coding for a mutant CDR3 region
US-09-822-698A-62

  Query Match             0.7%;  Score 20.2;  DB 10;  Length 48;
  Best Local Similarity   75.8%;  Pred. No. 3.8e+04;
  Matches   25;  Conservative    0;  Mismatches    8;  Indels    0;  Gaps    0;

Qy      45 GGAGCGGGCGAGAAGCTGCCGCCGAACGACAGG 77
           || | |||| |||||||||  || | || || ||
Db      13 GGGGGGGGCCAGAAGCTGCAGCTGGACTACTGG 45


RESULT 11
US-10-103-906-4/c
; Sequence 4, Application US/10103906
; Patent No. US20020156268A1
; GENERAL INFORMATION:
;  APPLICANT: Krotz, Achim H.
;  APPLICANT:  McElroy, Bethany M.
;  TITLE OF INVENTION: Methods for Removing Dimethoxytrityl Groups From
;  TITLE OF INVENTION:  Oligonucleotides
;  FILE REFERENCE: ISIS-3349
;  CURRENT APPLICATION NUMBER: US/10/103,906
;  CURRENT FILING DATE:  2002-03-22
;  PRIOR APPLICATION NUMBER: US/09/271,220
;  PRIOR FILING DATE: 1999-03-17
;  NUMBER OF SEQ ID NOS: 4
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: antisense sequence
US-10-103-906-4

  Query Match             0.7%;  Score 20;  DB 9;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 2.4e+04;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy    2484 AATGCATGTCACAGGCGGGA 2503
           ||||||||||||||||||||
Db      20 AATGCATGTCACAGGCGGGA 1


RESULT 12
US-10-078-949-3
; Sequence 3, Application US/10078949
; Patent No. US20020165189A1
; GENERAL INFORMATION:
;  APPLICANT: Crooke, Stanley T.
;  TITLE OF INVENTION: Oligoribonucleotides And Ribonucleases For Cleaving RNA
;  FILE REFERENCE: ISIS5027
;  CURRENT APPLICATION NUMBER: US/10/078,949
;  CURRENT FILING DATE:  2002-02-20
;  PRIOR APPLICATION NUMBER: 09/479,783
;  PRIOR FILING DATE: 2000-01-07
;  PRIOR APPLICATION NUMBER: 08/870,608
;  PRIOR FILING DATE: 1997-06-06
;  PRIOR APPLICATION NUMBER: 08/659,440
;  PRIOR FILING DATE: 1996-06-06
;  NUMBER OF SEQ ID NOS: 9
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
;   LENGTH: 20
;   TYPE: RNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Oligonucleotide
US-10-078-949-3

  Query Match             0.7%;  Score 20;  DB 9;  Length 20;
  Best Local Similarity   85.0%;  Pred. No. 2.4e+04;
  Matches   17;  Conservative    3;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 CCGAATGTGACCGCCTCCCG 20
           |||||:|:|||||||:||||
Db       1 CCGAAUGUGACCGCCUCCCG 20


RESULT 13
US-10-078-949-5
; Sequence 5, Application US/10078949
; Patent No. US20020165189A1
; GENERAL INFORMATION:
;  APPLICANT: Crooke, Stanley T.
;  TITLE OF INVENTION: Oligoribonucleotides And Ribonucleases For Cleaving RNA
;  FILE REFERENCE: ISIS5027
;  CURRENT APPLICATION NUMBER: US/10/078,949
;  CURRENT FILING DATE:  2002-02-20
;  PRIOR APPLICATION NUMBER: 09/479,783
;  PRIOR FILING DATE: 2000-01-07
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;  PRIOR APPLICATION NUMBER: 08/870,608
;  PRIOR FILING DATE: 1997-06-06
;  PRIOR APPLICATION NUMBER: 08/659,440
;  PRIOR FILING DATE: 1996-06-06
;  NUMBER OF SEQ ID NOS: 9
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 5
;   LENGTH: 20
;   TYPE: RNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Oligonucleotide
US-10-078-949-5

  Query Match             0.7%;  Score 20;  DB 9;  Length 20;
  Best Local Similarity   85.0%;  Pred. No. 2.4e+04;
  Matches   17;  Conservative    3;  Mismatches    0;  Indels    0;  Gaps    0;

Qy     127 TCAATGGAGCACATACAGGG 146
           :|||:||||||||:||||||
Db       1 UCAAUGGAGCACAUACAGGG 20


RESULT 14
US-10-078-949-7
; Sequence 7, Application US/10078949
; Patent No. US20020165189A1
; GENERAL INFORMATION:
;  APPLICANT: Crooke, Stanley T.
;  TITLE OF INVENTION: Oligoribonucleotides And Ribonucleases For Cleaving RNA
;  FILE REFERENCE: ISIS5027
;  CURRENT APPLICATION NUMBER: US/10/078,949
;  CURRENT FILING DATE:  2002-02-20
;  PRIOR APPLICATION NUMBER: 09/479,783
;  PRIOR FILING DATE: 2000-01-07
;  PRIOR APPLICATION NUMBER: 08/870,608
;  PRIOR FILING DATE: 1997-06-06
;  PRIOR APPLICATION NUMBER: 08/659,440
;  PRIOR FILING DATE: 1996-06-06
;  NUMBER OF SEQ ID NOS: 9
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 7
;   LENGTH: 20
;   TYPE: RNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Oligonucleotide
US-10-078-949-7

  Query Match             0.7%;  Score 20;  DB 9;  Length 20;
  Best Local Similarity   85.0%;  Pred. No. 2.4e+04;
  Matches   17;  Conservative    3;  Mismatches    0;  Indels    0;  Gaps    0;

Qy    2484 AATGCATGTCACAGGCGGGA 2503
           ||:|||:|:||||||||||
Db       1 AAUGCAUGUCACAGGCGGGA 20


RESULT 15
US-09-835-371-37/c
; Sequence 37, Application US/09835371
; Publication No. US20020187473A1
; GENERAL INFORMATION:
;  APPLICANT: UHLMANN, Eugen
;  APPLICANT:  BREIPOHL, Gerhard
;  APPLICANT:  WILL, David W
;  TITLE OF INVENTION: POLYAMIDE NUCLEIC ACID DERIVATIVES, AND AGENTS AND
;  TITLE OF INVENTION:  PROCESSES FOR PREPARING THEM
;  FILE REFERENCE: 02481.1743 SEQUENCE LISTING
;  CURRENT APPLICATION NUMBER: US/09/835,371
;  CURRENT FILING DATE:  2001-04-17
;  NUMBER OF SEQ ID NOS: 53
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 37
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:  base sequence
;   OTHER INFORMATION: of PNA targeting CMV
US-09-835-371-37

  Query Match             0.7%;  Score 20;  DB 9;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 2.4e+04;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy    2484 AATGCATGTCACAGGCGGGA 2503
           ||||||||||||||||||||
Db      20 AATGCATGTCACAGGCGGGA 1


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GenCore version 5.1.4_p5_4578

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Title: US-10-057-550A-64
Perfect score: 2977
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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 24791104 seqs, 12571243825 residues

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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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27: /cgn2_6/ptodata/1/pna/US096E_COMB.seq:*
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31: /cgn2_6/ptodata/1/pna/US098A_COMB.seq:*
32: /cgn2_6/ptodata/1/pna/US098B_COMB.seq:*
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34: /cgn2_6/ptodata/1/pna/US099A_COMB.seq:*
35: /cgn2_6/ptodata/1/pna/US099B_COMB.seq:*
36: /cgn2_6/ptodata/1/pna/US099C_COMB.seq:*
37: /cgn2_6/ptodata/1/pna/US099D_COMB.seq:*
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41: /cgn2_6/ptodata/1/pna/US101B_COMB.seq:*
42: /cgn2_6/ptodata/1/pna/US102A_COMB.seq:*
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46: /cgn2_6/ptodata/1/pna/US6002_COMB.seq:*
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48: /cgn2_6/ptodata/1/pna/US6004_COMB.seq:*
49: /cgn2_6/ptodata/1/pna/US6005_COMB.seq:*
50: /cgn2_6/ptodata/1/pna/US6006_COMB.seq:*
51: /cgn2_6/ptodata/1/pna/US6007_COMB.seq:*
52: /cgn2_6/ptodata/1/pna/US6008_COMB.seq:*
53: /cgn2_6/ptodata/1/pna/US6009_COMB.seq:*
54: /cgn2_6/ptodata/1/pna/US6010_COMB.seq:*
55: /cgn2_6/ptodata/1/pna/US6011_COMB.seq:*
56: /cgn2_6/ptodata/1/pna/US6012_COMB.seq:*
57: /cgn2_6/ptodata/1/pna/US6013_COMB.seq:*
58: /cgn2_6/ptodata/1/pna/US6014_COMB.seq:*
59: /cgn2_6/ptodata/1/pna/US6015_COMB.seq:*
60: /cgn2_6/ptodata/1/pna/US6016_COMB.seq:*
61: /cgn2_6/ptodata/1/pna/US6017_COMB.seq:*
62: /cgn2_6/ptodata/1/pna/US6018_COMB.seq:*
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64: /cgn2_6/ptodata/1/pna/US6020_COMB.seq:*
65: /cgn2_6/ptodata/1/pna/US6021_COMB.seq:*
66: /cgn2_6/ptodata/1/pna/US6022_COMB.seq:*
67: /cgn2_6/ptodata/1/pna/US6023_COMB.seq:*
68: /cgn2_6/ptodata/1/pna/US6024_COMB.seq:*
69: /cgn2_6/ptodata/1/pna/US6025_COMB.seq:*
70: /cgn2_6/ptodata/1/pna/US6026_COMB.seq:*
71: /cgn2_6/ptodata/1/pna/US6027_COMB.seq:*
72: /cgn2_6/ptodata/1/pna/US6028_COMB.seq:*
73: /cgn2_6/ptodata/1/pna/US6029_COMB.seq:*
74: /cgn2_6/ptodata/1/pna/US6030_COMB.seq:*
75: /cgn2_6/ptodata/1/pna/US6031_COMB.seq:*
76: /cgn2_6/ptodata/1/pna/US6032_COMB.seq:*
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78: /cgn2_6/ptodata/1/pna/US6034_COMB.seq:*
79: /cgn2_6/ptodata/1/pna/US6035_COMB.seq:*
80: /cgn2_6/ptodata/1/pna/US6036_COMB.seq:*
81: /cgn2_6/ptodata/1/pna/US6037_COMB.seq:*
82: /cgn2_6/ptodata/1/pna/US6038_COMB.seq:*
83: /cgn2_6/ptodata/1/pna/US6039_COMB.seq:*
84: /cgn2_6/ptodata/1/pna/US6040_COMB.seq:*
85: /cgn2_6/ptodata/1/pna/US6041_COMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
c	1	50	1.7	50	1	PCT-US01-47856-3119	Sequence 3119, Ap
c	2	50	1.7	50	40	US-10-131-827-3119	Sequence 3119, Ap
c	3	50	1.7	50	40	US-10-131-831-3119	Sequence 3119, Ap
	4	31.6	1.1	48	69	US-60-253-651-9462	Sequence 9462, Ap
	5	30.6	1.0	31	31	US-09-801-274-835	Sequence 835, App
	6	30.6	1.0	46	69	US-60-253-653-25508	Sequence 25508, A
	7	28	0.9	28	16	US-09-225-201B-979	Sequence 979, App
c	8	26	0.9	26	7	US-08-306-691-5	Sequence 5, Appli
	9	26	0.9	26	7	US-08-306-691-6	Sequence 6, Appli
c	10	26	0.9	26	12	US-08-821-015-5	Sequence 5, Appli
	11	26	0.9	26	12	US-08-821-015-6	Sequence 6, Appli
c	12	26	0.9	26	16	US-09-225-201B-980	Sequence 980, App
c	13	25	0.8	25	17	US-09-354-109-2	Sequence 2, Appli
	14	25	0.8	25	17	US-09-396-196F-44994	Sequence 44994, A
	15	25	0.8	25	17	US-09-396-196F-44995	Sequence 44995, A
	16	25	0.8	25	17	US-09-396-196F-44996	Sequence 44996, A
	17	25	0.8	25	17	US-09-396-196F-44997	Sequence 44997, A
	18	25	0.8	25	17	US-09-396-196F-44998	Sequence 44998, A
	19	25	0.8	25	17	US-09-396-196F-44999	Sequence 44999, A
	20	25	0.8	25	17	US-09-396-196F-45000	Sequence 45000, A
	21	25	0.8	25	17	US-09-396-196F-45001	Sequence 45001, A

22	25	0.8	25	17	US-09-396-196F-45002	Sequence 45002, A
23	25	0.8	25	17	US-09-396-196F-45003	Sequence 45003, A
24	25	0.8	25	17	US-09-396-196F-45004	Sequence 45004, A
25	25	0.8	25	17	US-09-396-196F-45005	Sequence 45005, A
26	25	0.8	25	17	US-09-396-196F-45006	Sequence 45006, A
27	25	0.8	25	17	US-09-396-196F-45007	Sequence 45007, A
28	25	0.8	25	17	US-09-396-196F-45008	Sequence 45008, A
29	25	0.8	25	17	US-09-396-196F-45009	Sequence 45009, A
30	25	0.8	25	17	US-09-396-196F-45010	Sequence 45010, A
31	25	0.8	25	17	US-09-396-196F-45011	Sequence 45011, A
32	25	0.8	25	17	US-09-396-196F-45012	Sequence 45012, A
33	25	0.8	25	17	US-09-396-196F-45013	Sequence 45013, A
34	25	0.8	25	17	US-09-396-196F-59148	Sequence 59148, A
35	25	0.8	25	17	US-09-396-196F-59150	Sequence 59150, A
36	25	0.8	25	17	US-09-396-196F-59151	Sequence 59151, A
37	25	0.8	25	17	US-09-396-196F-59152	Sequence 59152, A
38	25	0.8	25	17	US-09-396-196G-44994	Sequence 44994, A
39	25	0.8	25	17	US-09-396-196G-44995	Sequence 44995, A
40	25	0.8	25	17	US-09-396-196G-44996	Sequence 44996, A
41	25	0.8	25	17	US-09-396-196G-44997	Sequence 44997, A
42	25	0.8	25	17	US-09-396-196G-44998	Sequence 44998, A
43	25	0.8	25	17	US-09-396-196G-44999	Sequence 44999, A
44	25	0.8	25	17	US-09-396-196G-45000	Sequence 45000, A
45	25	0.8	25	17	US-09-396-196G-45001	Sequence 45001, A

ALIGNMENTS

```
RESULT 1
PCT-US01-47856-3119/c
; Sequence 3119, Application PC/TUS0147856
; GENERAL INFORMATION:
;  APPLICANT: BIOCARDIA, INC.
;  APPLICANT:  Wohlgemuth, Jay
;  APPLICANT:  Quertermous, Thomas
;  APPLICANT:  Johnson, Frances
;  APPLICANT:  Fry, Kirk
;  APPLICANT:  Matcuk, George
;  APPLICANT:  Prentice, James
;  APPLICANT:  Phillips, Julie
;  APPLICANT:  Woodward, Robert
;  APPLICANT:  Ly, Ngoc
;  APPLICANT:  Altman, Peter
;  TITLE OF INVENTION: LEUKOCYTE EXPRESSION PROFILING
;  FILE REFERENCE: 506612000140
;  CURRENT APPLICATION NUMBER: PCT/US01/47856
;  CURRENT FILING DATE:  2001-10-22
;  PRIOR APPLICATION NUMBER: US 60/241,994
;  PRIOR FILING DATE: 2000-10-20
;  PRIOR APPLICATION NUMBER: US 60/296,764
;  PRIOR FILING DATE: 2001-06-08
;  NUMBER OF SEQ ID NOS: 8832
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3119
;   LENGTH: 50
;   TYPE: DNA
;   ORGANISM: Homo sapiens
PCT-US01-47856-3119

  Query Match             1.7%;  Score 50;  DB 1;  Length 50;
  Best Local Similarity   100.0%;  Pred. No. 0.017;
  Matches   50;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy   2899 TTGTTTTTATTGCACCTGACAAAATACAGTTATCTGATGGTCCCTCAATT 2948
          ||||||||||||||||||||||||||||||||||||||||||||||||||
Db     50 TTGTTTTTATTGCACCTGACAAAATACAGTTATCTGATGGTCCCTCAATT 1


RESULT 2
US-10-131-827-3119/c
; Sequence 3119, Application US/10131827
; GENERAL INFORMATION:
;  APPLICANT: Wohlgemuth, Jay
;  APPLICANT:  Fry, Kirk
;  APPLICANT:  Woodward, Robert
;  APPLICANT:  Ly, Ngoc
;  TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING AND MONITORING AUTOIMM
;  TITLE OF INVENTION:  CHRONIC INFLAMMATORY DISEASES
;  FILE REFERENCE: 506612000120
;  CURRENT APPLICATION NUMBER: US/10/131,827
;  CURRENT FILING DATE:  2002-09-06
;  PRIOR APPLICATION NUMBER: US 10/006,290
;  PRIOR FILING DATE: 2001-10-22
;  PRIOR APPLICATION NUMBER: US 60/296,764
;  PRIOR FILING DATE: 2001-06-08
;  NUMBER OF SEQ ID NOS: 9090
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3119
;   LENGTH: 50
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-131-827-3119

  Query Match             1.7%;  Score 50;  DB 40;  Length 50;
  Best Local Similarity   100.0%;  Pred. No. 0.017;
  Matches   50;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy   2899 TTGTTTTTATTGCACCTGACAAAATACAGTTATCTGATGGTCCCTCAATT 2948
          ||||||||||||||||||||||||||||||||||||||||||||||||||
Db     50 TTGTTTTTATTGCACCTGACAAAATACAGTTATCTGATGGTCCCTCAATT 1


RESULT 3
US-10-131-831-3119/c
; Sequence 3119, Application US/10131831
; GENERAL INFORMATION:
;  APPLICANT: Wohlgemuth, Jay
;  APPLICANT:  Fry, Kirk
;  APPLICANT:  Woodward, Robert
;  APPLICANT:  Ly, Ngoc
;  TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING AND MONITORING
;  TITLE OF INVENTION:  TRANSPLANT REJECTION
;  FILE REFERENCE: 506612000121
;  CURRENT APPLICATION NUMBER: US/10/131,831
;  CURRENT FILING DATE:  2002-08-05
;  PRIOR APPLICATION NUMBER: US 10/006,290
;  PRIOR FILING DATE: 2001-10-22
;  PRIOR APPLICATION NUMBER: US 60/296,764
;  PRIOR FILING DATE: 2001-06-08
;  NUMBER OF SEQ ID NOS: 9190
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3119
;   LENGTH: 50
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-131-831-3119

  Query Match             1.7%;  Score 50;  DB 40;  Length 50;
  Best Local Similarity   100.0%;  Pred. No. 0.017;
  Matches   50;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy   2899 TTGTTTTTATTGCACCTGACAAAATACAGTTATCTGATGGTCCCTCAATT 2948
          ||||||||||||||||||||||||||||||||||||||||||||||||||
Db     50 TTGTTTTTATTGCACCTGACAAAATACAGTTATCTGATGGTCCCTCAATT 1


RESULT 4
US-60-253-651-9462
; Sequence 9462, Application US/60253651
; GENERAL INFORMATION:
;  APPLICANT: Glenn, Mattew
;  APPLICANT:  Grigor, Murray R
;  TITLE OF INVENTION: Compositions isolated from bovine tissue
;  TITLE OF INVENTION:  and methods for their use.
;  FILE REFERENCE: 1055P3
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;  CURRENT APPLICATION NUMBER: US/60/253,651
;  CURRENT FILING DATE:  2000-11-28
;  NUMBER OF SEQ ID NOS: 27858
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 9462
;   LENGTH: 48
;   TYPE: DNA
;   ORGANISM: Bovine
US-60-253-651-9462

  Query Match             1.1%;  Score 31.6;  DB 69;  Length 48;
  Best Local Similarity   80.4%;  Pred. No. 1.5e+03;
  Matches   37;  Conservative    0;  Mismatches    9;  Indels    0;  Gaps    0;

Qy   1688 AGGATAACAACCCATTCAGTTTCCAGTCGGATGTCTACTCCTATGG 1733
          ||||    ||||| | ||| |||||||| |||||||| |||||||
Db      2 AGGACCCGAACCCCTACAGCTTCCAGTCAGATGTCTACGCCTATGG 47


RESULT 5
US-09-801-274-835
; Sequence 835, Application US/09801274
; GENERAL INFORMATION:
;  APPLICANT: Cargill, Michele
;  APPLICANT:  Ireland, James S.
;  APPLICANT:  Lander, Eric S.
;  TITLE OF INVENTION: HUMAN SINGLE NUCLEOTIDE POLYMORPHISMS
;  FILE REFERENCE: 2825.2009-001
;  CURRENT APPLICATION NUMBER: US/09/801,274
;  CURRENT FILING DATE:  2001-03-07
;  PRIOR APPLICATION NUMBER: US 60/187,510
;  PRIOR FILING DATE: 2000-03-07
;  PRIOR APPLICATION NUMBER: US 60/206,129
;  PRIOR FILING DATE: 2000-05-22
;  NUMBER OF SEQ ID NOS: 1802
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 835
;   LENGTH: 31
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-801-274-835

  Query Match             1.0%;  Score 30.6;  DB 31;  Length 31;
  Best Local Similarity   96.8%;  Pred. No. 2.3e+03;
  Matches   30;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy   2144 CCCTTTCTCCAGAGGCAGAACACATGTTTTC 2174
          |||||||||||||||:|||||||||||||||
Db      1 CCCTTTCTCCAGAGGYAGAACACATGTTTTC 31


RESULT 6
US-60-253-653-25508
; Sequence 25508, Application US/60253653
; GENERAL INFORMATION:
;  APPLICANT: Glenn, Matthew
;  TITLE OF INVENTION: Compositions isolated from ovine tissues
;  TITLE OF INVENTION:  and methods for their use.
;  FILE REFERENCE: 1057P
;  CURRENT APPLICATION NUMBER: US/60/253,653
;  CURRENT FILING DATE:  2000-11-28
;  NUMBER OF SEQ ID NOS: 30124
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 25508
;   LENGTH: 46
;   TYPE: DNA
;   ORGANISM: Ovine
US-60-253-653-25508

  Query Match             1.0%;  Score 30.6;  DB 69;  Length 46;
  Best Local Similarity   80.0%;  Pred. No. 2.8e+03;
  Matches   36;  Conservative    0;  Mismatches    9;  Indels    0;  Gaps    0;

Qy   1184 CCACTCGGATTGGGTCAGGCTCTTTTGGAACTGTTTATAAGGGTA 1228
          ||||||  ||||| ||| |||| || || ||||||||||| || |
Db      2 CCACTCCCATTGGATCACGCTCCTTCGGGACTGTTTATAACGGCA 46


RESULT 7
US-09-225-201B-979
; Sequence 979, Application US/09225201B
;  GENERAL INFORMATION:
;       APPLICANT: Chenchik, Alex
;                  Jokhadze, George
;                  Bibilashvilli, Robert
;       TITLE OF INVENTION: METHOD OF ASSAYING DIFFERENTIAL
;                           EXPRESSION
;       NUMBER OF SEQUENCES: 1375
;       CORRESPONDENCE ADDRESS:
;            ADDRESSEE: Fish & Richardson, P.C.
;            STREET: 2200 Sand Hill Road, Suite 100
;            CITY: Menlo Park
;            STATE: CA
;            COUNTRY: US
;            ZIP: 94025
;       COMPUTER READABLE FORM:
;            MEDIUM TYPE: Diskette
;            COMPUTER: IBM Compatible
;            OPERATING SYSTEM: Windows95
;            SOFTWARE: FastSEQ for Windows Version 2.0
;       CURRENT APPLICATION DATA:
;            APPLICATION NUMBER: US/09/225,201B
;            FILING DATE: 05-Jan-1999
;            CLASSIFICATION: <Unknown>
;       PRIOR APPLICATION DATA:
;            APPLICATION NUMBER: US/08/859,998
;            FILING DATE: 21-MAY-1997
;       ATTORNEY/AGENT INFORMATION:
;            NAME: Field, Bret E.
;            REGISTRATION NUMBER: 37,620
;            REFERENCE/DOCKET NUMBER: 09096/002001
;       TELECOMMUNICATION INFORMATION:
;            TELEPHONE: 415-322-5070
;            TELEFAX: 415-854-0875
;  INFORMATION FOR SEQ ID NO: 979:
;       SEQUENCE CHARACTERISTICS:
;            LENGTH: 28 base pairs
;            TYPE: nucleic acid
;            STRANDEDNESS: single
;            TOPOLOGY: linear
;       MOLECULE TYPE: DNA
;       FEATURE:
;            OTHER INFORMATION:  oligonucleotide primer
;       SEQUENCE DESCRIPTION: SEQ ID NO: 979:
US-09-225-201B-979

  Query Match             0.9%;  Score 28;  DB 16;  Length 28;
  Best Local Similarity   100.0%;  Pred. No. 1.1e+04;
  Matches   28;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy   1704 CAGTTTCCAGTCGGATGTCTACTCCTAT 1731
          ||||||||||||||||||||||||||||
Db      1 CAGTTTCCAGTCGGATGTCTACTCCTAT 28


RESULT 8
US-08-306-691-5/c
; Sequence 5, Application US/08306691
;  GENERAL INFORMATION:
;    APPLICANT:  Calabretta, Bruno
;    APPLICANT:  Skorski, Tomasz
;    TITLE OF INVENTION:  ANTISENSE
;    TITLE OF INVENTION:  OLIGONUCLEOTIDES TARGETING COOPERATING ONCOGENES
;    NUMBER OF SEQUENCES:  12
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Seidel, Gonda, Lavorgna & Monaco, P.C.
```

```
;       STREET:  Two Penn Center, Suite 1800
;       CITY:  Philadelphia
;       STATE:  Pennsylvania
;       COUNTRY:  U.S.A.
;       ZIP:  19102
;     COMPUTER READABLE FORM:
;       MEDIUM TYPE:  Diskette, 3.50 inch, 720 Kb
;       COMPUTER:  IBM PS/2
;       OPERATING SYSTEM:  MS-DOS
;       SOFTWARE:  WordPerfect 5.1
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  US/08/306,691
;       FILING DATE:
;       CLASSIFICATION:  514
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:
;       FILING DATE:
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  Monaco, Daniel A.
;       REGISTRATION NUMBER:  30,480
;       REFERENCE/DOCKET NUMBER:  8321-8
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  (215) 568-8383
;       TELEFAX:  (215) 568-5549
;       TELEX:  None
;   INFORMATION FOR SEQ ID NO:  5:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  26 Nucleotides
;       TYPE:  nucleic acid
;       STRANDEDNESS:  single stranded
;       TOPOLOGY:  linear
US-08-306-691-5

  Query Match             0.9%;  Score 26;  DB 7;  Length 26;
  Best Local Similarity   100.0%;  Pred. No. 3.6e+04;
  Matches   26;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       5 ATGTGACCGCCTCCCGCTCCCTCACC 30
           ||||||||||||||||||||||||||
Db      26 ATGTGACCGCCTCCCGCTCCCTCACC 1


RESULT 9
US-08-306-691-6
; Sequence 6, Application US/08306691
;  GENERAL INFORMATION:
;    APPLICANT:  Calabretta, Bruno
;    APPLICANT:  Skorski, Tomasz
;    TITLE OF INVENTION:  ANTISENSE
;    TITLE OF INVENTION:  OLIGONUCLEOTIDES TARGETING COOPERATING ONCOGENES
;    NUMBER OF SEQUENCES:  12
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Seidel, Gonda, Lavorgna & Monaco, P.C.
;      STREET:  Two Penn Center, Suite 1800
;      CITY:  Philadelphia
;      STATE:  Pennsylvania
;      COUNTRY:  U.S.A.
;      ZIP:  19102
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette, 3.50 inch, 720 Kb
;      COMPUTER:  IBM PS/2
;      OPERATING SYSTEM:  MS-DOS
;      SOFTWARE:  WordPerfect 5.1
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/306,691
;      FILING DATE:
;      CLASSIFICATION:  514
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Monaco, Daniel A.
;      REGISTRATION NUMBER:  30,480
;      REFERENCE/DOCKET NUMBER:  8321-8
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (215) 568-8383
;      TELEFAX:  (215) 568-5549
;      TELEX:  None
;  INFORMATION FOR SEQ ID NO:  6:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  26 Nucleotides
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single stranded
;      TOPOLOGY:  linear
US-08-306-691-6

  Query Match             0.9%;  Score 26;  DB 7;  Length 26;
  Best Local Similarity   100.0%;  Pred. No. 3.6e+04;
  Matches   26;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       5 ATGTGACCGCCTCCCGCTCCCTCACC 30
           ||||||||||||||||||||||||||
Db       1 ATGTGACCGCCTCCCGCTCCCTCACC 26


RESULT 10
US-08-821-015-5/c
; Sequence 5, Application US/08821015
;  GENERAL INFORMATION:
;    APPLICANT:  Calabretta, Bruno
;    APPLICANT:  Skorski, Tomasz
;    TITLE OF INVENTION:  METHOD FOR INHIBITING NEOPLASTIC CELL
;    TITLE OF INVENTION:  PROLIFERATION WITH ANTISENSE OLIGONUCLEOTIDES TARGETING COO
;    NUMBER OF SEQUENCES:  55
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Seidel, Gonda, Lavorgna & Monaco, P.C.
;      STREET:  Two Penn Center, Suite 1800
;      CITY:  Philadelphia
;      STATE:  Pennsylvania
;      COUNTRY:  U.S.A.
;      ZIP:  19102
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette, 3.50 inch, 720 Kb
;      COMPUTER:  IBM PS/2
;      OPERATING SYSTEM:  MS-DOS
;      SOFTWARE:  WordPerfect 5.1
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/821,015
;      FILING DATE:
;      CLASSIFICATION:  536
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/306,691
;      FILING DATE:  September 15, 1994
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Monaco, Daniel A.
;      REGISTRATION NUMBER:  30,480
;      REFERENCE/DOCKET NUMBER:  8321-8 DI1
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (215) 568-8383
;      TELEFAX:  (215) 568-5549
;      TELEX:  None
;  INFORMATION FOR SEQ ID NO:  5:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  26 Nucleotides
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single stranded
;      TOPOLOGY:  linear
US-08-821-015-5

  Query Match             0.9%;  Score 26;  DB 12;  Length 26;
  Best Local Similarity   100.0%;  Pred. No. 3.6e+04;
  Matches   26;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       5 ATGTGACCGCCTCCCGCTCCCTCACC 30
           ||||||||||||||||||||||||||
Db      26 ATGTGACCGCCTCCCGCTCCCTCACC 1
```

```
RESULT 11
US-08-821-015-6
; Sequence 6, Application US/08821015
;  GENERAL INFORMATION:
;    APPLICANT:  Calabretta, Bruno
;    APPLICANT:  Skorski, Tomasz
;    TITLE OF INVENTION:  METHOD FOR INHIBITING NEOPLASTIC CELL
;    TITLE OF INVENTION:  PROLIFERATION WITH ANTISENSE OLIGONUCLEOTIDES TARGETING COOPER
;    NUMBER OF SEQUENCES:  55
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Seidel, Gonda, Lavorgna & Monaco, P.C.
;      STREET:  Two Penn Center, Suite 1800
;      CITY:  Philadelphia
;      STATE:  Pennsylvania
;      COUNTRY:  U.S.A.
;      ZIP:  19102
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette, 3.50 inch, 720 Kb
;      COMPUTER:  IBM PS/2
;      OPERATING SYSTEM:  MS-DOS
;      SOFTWARE:  WordPerfect 5.1
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/821,015
;      FILING DATE:
;      CLASSIFICATION:  536
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/306,691
;      FILING DATE:  September 15, 1994
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Monaco, Daniel A.
;      REGISTRATION NUMBER:  30,480
;      REFERENCE/DOCKET NUMBER:  8321-8 DI1
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (215) 568-8383
;      TELEFAX:  (215) 568-5549
;      TELEX:  None
;  INFORMATION FOR SEQ ID NO:  6:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  26 Nucleotides
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single stranded
;      TOPOLOGY:  linear
US-08-821-015-6

  Query Match             0.9%;  Score 26;  DB 12;  Length 26;
  Best Local Similarity   100.0%;  Pred. No. 3.6e+04;
  Matches   26;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       5 ATGTGACCGCCTCCCGCTCCCTCACC 30
           ||||||||||||||||||||||||||
Db       1 ATGTGACCGCCTCCCGCTCCCTCACC 26


RESULT 12
US-09-225-201B-980/c
; Sequence 980, Application US/09225201B
;   GENERAL INFORMATION:
;        APPLICANT: Chenchik, Alex
;                   Jokhadze, George
;                   Bibilashvilli, Robert
;        TITLE OF INVENTION: METHOD OF ASSAYING DIFFERENTIAL
;                            EXPRESSION
;        NUMBER OF SEQUENCES: 1375
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Fish & Richardson, P.C.
;             STREET: 2200 Sand Hill Road, Suite 100
;             CITY: Menlo Park
;             STATE: CA
;             COUNTRY: US
;             ZIP: 94025
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Diskette
;             COMPUTER: IBM Compatible
;             OPERATING SYSTEM: Windows95
;             SOFTWARE: FastSEQ for Windows Version 2.0
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/09/225,201B
;             FILING DATE: 05-Jan-1999
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: US/08/859,998
;             FILING DATE: 21-MAY-1997
;        ATTORNEY/AGENT INFORMATION:
;             NAME: Field, Bret E.
;             REGISTRATION NUMBER: 37,620
;             REFERENCE/DOCKET NUMBER: 09096/002001
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: 415-322-5070
;             TELEFAX: 415-854-0875
;   INFORMATION FOR SEQ ID NO: 980:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 26 base pairs
;             TYPE: nucleic acid
;             STRANDEDNESS: single
;             TOPOLOGY: linear
;        MOLECULE TYPE: DNA
;        FEATURE:
;             OTHER INFORMATION:  oligonucleotide primer
;        SEQUENCE DESCRIPTION: SEQ ID NO: 980:
US-09-225-201B-980

  Query Match             0.9%;  Score 26;  DB 16;  Length 26;
  Best Local Similarity   100.0%;  Pred. No. 3.6e+04;
  Matches   26;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy    1963 TCTCTACCGAAGATCAACCGGAGCGC 1988
           ||||||||||||||||||||||||||
Db      26 TCTCTACCGAAGATCAACCGGAGCGC 1


RESULT 13
US-09-354-109-2/c
; Sequence 2, Application US/09354109
;  GENERAL INFORMATION:
;    APPLICANT:  Kasid, Usha
;    APPLICANT:  Gokhale, Prafulla
;    APPLICANT:  Dritschilo, Anatoly
;    APPLICANT:  Rahman, Aqulur
;    TITLE OF INVENTION:  Liposomes contaiing Oligonucelotides
;    NUMBER OF SEQUENCES:  3
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Hendricks and Assoc.
;      STREET:  P.O. Box 2509
;      CITY:  Fairfax
;      STATE:  VA
;      COUNTRY:  US
;      ZIP:  22031
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/354,109
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/957,327
;      FILING DATE:  24-OCT-1997
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Hendricks, Glenna
;      REGISTRATION NUMBER:  32,535
;      REFERENCE/DOCKET NUMBER:  kasid
;    TELECOMMUNICATION INFORMATION:
```

```
;       TELEPHONE:  (703) 591-4470
;       TELEFAX:  (703) 591-4428
;   INFORMATION FOR SEQ ID NO:  2:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  25 base pairs
;       TYPE:  nucleic acid
;       STRANDEDNESS:  single
;       TOPOLOGY:  unknown
;     MOLECULE TYPE:  DNA (genomic)
;     HYPOTHETICAL:  NO
;     ANTI-SENSE:  YES
US-09-354-109-2

  Query Match             0.8%;  Score 25;  DB 17;  Length 25;
  Best Local Similarity   100.0%;  Pred. No. 6.5e+04;
  Matches   25;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy     121 GCTGCATCAATGGAGCACATACAGG 145
           |||||||||||||||||||||||||
Db      25 GCTGCATCAATGGAGCACATACAGG 1


RESULT 14
US-09-396-196F-44994
; Sequence 44994, Application US/09396196F
; GENERAL INFORMATION:
;  APPLICANT: Michael Mittmann
;  APPLICANT:  David Mack
;  APPLICANT:  David Lockhart
;  APPLICANT:  Affymetrix, Inc.
;  TITLE OF INVENTION: Methods of Genetic Analysis
;  FILE REFERENCE: 3101.1
;  CURRENT APPLICATION NUMBER: US/09/396,196F
;  CURRENT FILING DATE:  2001-09-15
;  PRIOR APPLICATION NUMBER: 60/100,678
;  PRIOR FILING DATE: 1998-09-17
;  NUMBER OF SEQ ID NOS: 127806
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 44994
;   LENGTH: 25
;   TYPE: DNA
;   ORGANISM: mus musculus
US-09-396-196F-44994

  Query Match             0.8%;  Score 25;  DB 17;  Length 25;
  Best Local Similarity   100.0%;  Pred. No. 6.5e+04;
  Matches   25;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy    1855 AACTGCCCCAAAGCAATGAAGAGGC 1879
           |||||||||||||||||||||||||
Db       1 AACTGCCCCAAAGCAATGAAGAGGC 25


RESULT 15
US-09-396-196F-44995
; Sequence 44995, Application US/09396196F
; GENERAL INFORMATION:
;  APPLICANT: Michael Mittmann
;  APPLICANT:  David Mack
;  APPLICANT:  David Lockhart
;  APPLICANT:  Affymetrix, Inc.
;  TITLE OF INVENTION: Methods of Genetic Analysis
;  FILE REFERENCE: 3101.1
;  CURRENT APPLICATION NUMBER: US/09/396,196F
;  CURRENT FILING DATE:  2001-09-15
;  PRIOR APPLICATION NUMBER: 60/100,678
;  PRIOR FILING DATE: 1998-09-17
;  NUMBER OF SEQ ID NOS: 127806
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 44995
;   LENGTH: 25
;   TYPE: DNA
;   ORGANISM: mus musculus
US-09-396-196F-44995

  Query Match             0.8%;  Score 25;  DB 17;  Length 25;
  Best Local Similarity   100.0%;  Pred. No. 6.5e+04;
  Matches   25;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy    1876 AGGCTGGTAGCTGACTGTGTGAAGA 1900
           |||||||||||||||||||||||||
Db       1 AGGCTGGTAGCTGACTGTGTGAAGA 25


Search completed: May 16, 2003, 12:16:27
Job time : 6348 secs
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GenCore version 5.1.4_p5_4578

OM nucleic - nucleic search, using sw model

Run on: May 16, 2003, 07:11:11 ; Search time 1366 Seconds
(without alignments)
11277.539 Million cell updates/sec

Title: US-10-057-550A-64
Perfect score: 2977
Sequence: 1 ccgaatgtgaccgcctcccg.....taataaaataaattaaattt 2977

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 6404235 seqs, 2587356060 residues

Total number of hits satisfying chosen parameters: 7758442

Minimum DB seq length: 0
Maximum DB seq length: 50

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Pending_Patents_NA_New:*
1: /cgn2_6/ptodata/2/pna/PCT_NEW_COMB.seq:*
2: /cgn2_6/ptodata/2/pna/US06_NEW_COMB.seq:*
3: /cgn2_6/ptodata/2/pna/US07_NEW_COMB.seq:*
4: /cgn2_6/ptodata/2/pna/US08_NEW_COMB.seq:*
5: /cgn2_6/ptodata/2/pna/US09_NEW_COMB.seq:*
6: /cgn2_6/ptodata/2/pna/US09_NEW_COMB.seq2:*
7: /cgn2_6/ptodata/2/pna/US09_NEW_COMB.seq3:*
8: /cgn2_6/ptodata/2/pna/US10_NEW_COMB.seq:*
9: /cgn2_6/ptodata/2/pna/US10_NEW_COMB.seq2:*
10: /cgn2_6/ptodata/2/pna/US60_NEW_COMB.seq:*
11: /cgn2_6/ptodata/2/pna/US60_NEW_COMB.seq2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
c	1	50	1.7	50	9	US-10-325-899-3119	Sequence 3119, Ap
c	2	25	0.8	25	8	US-10-075-994A-2	Sequence 2, Appli
	3	23.4	0.8	25	11	US-60-427-808-320641	Sequence 320641,
	4	23.4	0.8	25	11	US-60-427-808-556623	Sequence 556623,
	5	23.4	0.8	25	11	US-60-427-808-917222	Sequence 917222,
	6	23.4	0.8	25	11	US-60-427-836-397923	Sequence 397923,
c	7	23	0.8	50	9	US-10-325-899-5803	Sequence 5803, Ap
	8	22.4	0.8	43	11	US-60-434-832-1070	Sequence 1070, Ap
	9	22.2	0.7	45	11	US-60-288-292-19321	Sequence 19321, A
	10	22	0.7	22	9	US-10-293-338-4068	Sequence 4068, Ap
	11	22	0.7	47	9	US-10-349-143-3876	Sequence 3876, Ap
	12	21.8	0.7	25	1	PCT-US02-14877A-875	Sequence 875, App
	13	21.8	0.7	25	11	US-60-427-808-320640	Sequence 320640,
	14	21.8	0.7	25	11	US-60-427-808-556622	Sequence 556622,
	15	21.8	0.7	25	11	US-60-427-808-917221	Sequence 917221,
	16	21.8	0.7	25	11	US-60-427-836-397922	Sequence 397922,
	17	21.8	0.7	39	8	US-10-287-787-18691	Sequence 18691, A
c	18	21.8	0.7	39	8	US-10-287-787-18692	Sequence 18692, A
	19	21.8	0.7	39	8	US-10-287-787-18693	Sequence 18693, A
c	20	21.8	0.7	50	8	US-10-287-787-19984	Sequence 19984, A
c	21	21.6	0.7	50	6	US-09-912-293-210904	Sequence 210904,
c	22	21.6	0.7	50	9	US-10-325-899-4714	Sequence 4714, Ap
	23	21.4	0.7	25	11	US-60-427-808-116035	Sequence 116035,
	24	21.4	0.7	50	6	US-09-912-293-130705	Sequence 130705,
	25	21.2	0.7	46	8	US-10-287-787-4937	Sequence 4937, Ap
	26	21.2	0.7	47	8	US-10-287-787-4936	Sequence 4936, Ap
c	27	21.2	0.7	49	8	US-10-389-048-4355	Sequence 4355, Ap
c	28	21	0.7	44	8	US-10-287-787-19789	Sequence 19789, A
c	29	21	0.7	44	8	US-10-287-787-19790	Sequence 19790, A
c	30	21	0.7	47	9	US-10-349-143-2948	Sequence 2948, Ap
c	31	21	0.7	50	6	US-09-912-293-242736	Sequence 242736,
c	32	21	0.7	50	9	US-10-325-899-3101	Sequence 3101, Ap
c	33	21	0.7	50	9	US-10-325-899-8045	Sequence 8045, Ap
	34	20.8	0.7	25	11	US-60-427-808-506441	Sequence 506441,
	35	20.8	0.7	25	11	US-60-427-808-630023	Sequence 630023,
c	36	20.8	0.7	25	11	US-60-427-808-943561	Sequence 943561,
	37	20.8	0.7	25	11	US-60-427-836-451365	Sequence 451365,
c	38	20.8	0.7	50	9	US-10-325-899-7636	Sequence 7636, Ap
c	39	20.6	0.7	45	8	US-10-287-787-19197	Sequence 19197, A
c	40	20.6	0.7	50	6	US-09-912-293-43884	Sequence 43884, A
	41	20.6	0.7	50	9	US-10-325-899-1696	Sequence 1696, Ap
c	42	20.4	0.7	45	8	US-10-287-787-21968	Sequence 21968, A
	43	20.4	0.7	45	8	US-10-287-787-21970	Sequence 21970, A
c	44	20.4	0.7	50	9	US-10-325-899-3367	Sequence 3367, Ap
c	45	20.4	0.7	50	9	US-10-325-899-4603	Sequence 4603, Ap

ALIGNMENTS

RESULT 1
US-10-325-899-3119/c
; Sequence 3119, Application US/10325899
; GENERAL INFORMATION:
; APPLICANT: Wohlgemuth, Jay
; APPLICANT: Fry, Kirk
; APPLICANT: Ly, Ngoc
; APPLICANT: Woodward, Robert
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING AND MONITORING TRANSPL
; TITLE OF INVENTION: REJECTION
; FILE REFERENCE: 506612000122
; CURRENT APPLICATION NUMBER: US/10/325,899
; CURRENT FILING DATE: 2002-12-20
; PRIOR APPLICATION NUMBER: US 60/296,764
; PRIOR FILING DATE: 2001-06-08
; PRIOR APPLICATION NUMBER: US 10/006,290
; PRIOR FILING DATE: 2001-10-22
; PRIOR APPLICATION NUMBER: US 10/131,831
; PRIOR FILING DATE: 2002-04-24
; NUMBER OF SEQ ID NOS: 9966
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3119
; LENGTH: 50
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-325-899-3119

Query Match 1.7%; Score 50; DB 9; Length 50;
Best Local Similarity 100.0%; Pred. No. 0.00061;
Matches 50; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2899 TTGTTTTTATTGCACCTGACAAAATACAGTTATCTGATGGTCCCTCAATT 2948
||||||||||||||||||||||||||||||||||||||||||||||||||
Db 50 TTGTTTTTATTGCACCTGACAAAATACAGTTATCTGATGGTCCCTCAATT 1

RESULT 2
US-10-075-994A-2/c
; Sequence 2, Application US/10075994A
; GENERAL INFORMATION:
; APPLICANT: KASID, Usha
; APPLICANT: GOKHALE, Prafulla
; APPLICANT: PIE, Jin
; APPLICANT: MEWANI, Rajshree
; APPLICANT: AHMAD, Imran

```
;  APPLICANT:  DRITSCHILO, Anatoly
;  APPLICANT:  RAHMAN, Aquilur
;  TITLE OF INVENTION: CHEMOSENSITIZING WITH LIPOSOMES CONTAINING OLIGONUCLEOTIDES
;  FILE REFERENCE: 219604
;  CURRENT APPLICATION NUMBER: US/10/075,994A
;  CURRENT FILING DATE:  2002-02-15
;  NUMBER OF SEQ ID NOS: 7
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2
;   LENGTH: 25
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Synthetic
US-10-075-994A-2

  Query Match             0.8%;  Score 25;  DB 8;  Length 25;
  Best Local Similarity   100.0%;  Pred. No. 8.2e+03;
  Matches   25;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy    121 GCTGCATCAATGGAGCACATACAGG 145
          |||||||||||||||||||||||||
Db     25 GCTGCATCAATGGAGCACATACAGG 1


RESULT 3
US-60-427-808-320641
; Sequence 320641, Application US/60427808
; GENERAL INFORMATION:
;  APPLICANT: Xue Mei Zhou
;  TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
;  FILE REFERENCE: 3528
;  CURRENT APPLICATION NUMBER: US/60/427,808
;  CURRENT FILING DATE:  2002-11-20
;  NUMBER OF SEQ ID NOS: 982914
;  SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 320641
;   LENGTH: 25
;   TYPE: DNA
;   ORGANISM: Mus musculus
US-60-427-808-320641

  Query Match             0.8%;  Score 23.4;  DB 11;  Length 25;
  Best Local Similarity   96.0%;  Pred. No. 2.4e+04;
  Matches   24;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy   2210 CAGGGCCTTAACTTCATGTTGCCTT 2234
          |||||||||||||||| |||||||
Db      1 CAGGGCCTTAACTTCATATTGCCTT 25


RESULT 4
US-60-427-808-556623
; Sequence 556623, Application US/60427808
; GENERAL INFORMATION:
;  APPLICANT: Xue Mei Zhou
;  TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
;  FILE REFERENCE: 3528
;  CURRENT APPLICATION NUMBER: US/60/427,808
;  CURRENT FILING DATE:  2002-11-20
;  NUMBER OF SEQ ID NOS: 982914
;  SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 556623
;   LENGTH: 25
;   TYPE: DNA
;   ORGANISM: Mus musculus
US-60-427-808-556623

  Query Match             0.8%;  Score 23.4;  DB 11;  Length 25;
  Best Local Similarity   96.0%;  Pred. No. 2.4e+04;
  Matches   24;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy   2214 GCCTTAACTTCATGTTGCCTTCTTT 2238
          |||||||||||| ||||||||||
Db      1 GCCTTAACTTCATATTGCCTTCTTT 25


RESULT 5
US-60-427-808-917222
; Sequence 917222, Application US/60427808
; GENERAL INFORMATION:
;  APPLICANT: Xue Mei Zhou
;  TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
;  FILE REFERENCE: 3528
;  CURRENT APPLICATION NUMBER: US/60/427,808
;  CURRENT FILING DATE:  2002-11-20
;  NUMBER OF SEQ ID NOS: 982914
;  SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 917222
;   LENGTH: 25
;   TYPE: DNA
;   ORGANISM: Mus musculus
US-60-427-808-917222

  Query Match             0.8%;  Score 23.4;  DB 11;  Length 25;
  Best Local Similarity   96.0%;  Pred. No. 2.4e+04;
  Matches   24;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy   2217 TTAACTTCATGTTGCCTTCTTTTCT 2241
          |||||||||| ||||||||||||||
Db      1 TTAACTTCATATTGCCTTCTTTTCT 25


RESULT 6
US-60-427-836-397923
; Sequence 397923, Application US/60427836
; GENERAL INFORMATION:
;  APPLICANT: Xue Mei Zhou
;  TITLE OF INVENTION: Methods of Genetic Analysis of Rat
;  FILE REFERENCE: 3527
;  CURRENT APPLICATION NUMBER: US/60/427,836
;  CURRENT FILING DATE:  2002-11-20
;  NUMBER OF SEQ ID NOS: 699466
;  SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 397923
;   LENGTH: 25
;   TYPE: DNA
;   ORGANISM: Rattus norvegicus
US-60-427-836-397923

  Query Match             0.8%;  Score 23.4;  DB 11;  Length 25;
  Best Local Similarity   96.0%;  Pred. No. 2.4e+04;
  Matches   24;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy   2214 GCCTTAACTTCATGTTGCCTTCTTT 2238
          |||||||||||| ||||||||||
Db      1 GCCTTAACTTCATATTGCCTTCTTT 25


RESULT 7
US-10-325-899-5803/c
; Sequence 5803, Application US/10325899
; GENERAL INFORMATION:
;  APPLICANT: Wohlgemuth, Jay
;  APPLICANT:  Fry, Kirk
;  APPLICANT:  Ly, Ngoc
;  APPLICANT:  Woodward, Robert
;  TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING AND MONITORING TRANSPL
;  TITLE OF INVENTION:  REJECTION
;  FILE REFERENCE: 506612000122
;  CURRENT APPLICATION NUMBER: US/10/325,899
;  CURRENT FILING DATE:  2002-12-20
;  PRIOR APPLICATION NUMBER: US 60/296,764
;  PRIOR FILING DATE: 2001-06-08
;  PRIOR APPLICATION NUMBER: US 10/006,290
;  PRIOR FILING DATE: 2001-10-22
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;  PRIOR APPLICATION NUMBER: US 10/131,831
;  PRIOR FILING DATE: 2002-04-24
;  NUMBER OF SEQ ID NOS: 9966
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 5803
;   LENGTH: 50
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-325-899-5803

  Query Match             0.8%;  Score 23;  DB 9;  Length 50;
  Best Local Similarity   74.4%;  Pred. No. 4.4e+04;
  Matches   29;  Conservative    0;  Mismatches   10;  Indels    0;  Gaps    0;

Qy   2661 GTGCATTGGGATGGTTTTCCAGGCAAGGCACTCGGCCAA 2699
          ||  |||| |||||||| ||||| |||| || ||   ||
Db     40 GTTTATTGAGATGGTTTCCCAGGAAAGGTACACGTTGAA 2


RESULT 8
US-60-434-832-1070
; Sequence 1070, Application US/60434832
; GENERAL INFORMATION:
;  APPLICANT: Roemer, Terry
;  APPLICANT:  Jiang, Bo
;  APPLICANT:  Boone, Charles
;  APPLICANT:  Bussey, Howard
;  TITLE OF INVENTION: Nucleic Acids Encoding Antifungal Drug Targets and Methods of Use
;  FILE REFERENCE: 10182-023-888
;  CURRENT APPLICATION NUMBER: US/60/434,832
;  CURRENT FILING DATE:  2002-12-19
;  NUMBER OF SEQ ID NOS: 7137
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1070
;   LENGTH: 43
;   TYPE: DNA
;   ORGANISM: Candida albicans
US-60-434-832-1070

  Query Match             0.8%;  Score 22.4;  DB 11;  Length 43;
  Best Local Similarity   72.5%;  Pred. No. 6.1e+04;
  Matches   29;  Conservative    0;  Mismatches   11;  Indels    0;  Gaps    0;

Qy   2799 CTAACAAACAAACAAACAAACAGCCTTGTTTCTCTAGTCA 2838
          | ||||||||||||||||||||  | | |   | ||  ||
Db      3 CAAACAAACAAACAAACAAACAAACGTATACATATACACA 42


RESULT 9
US-60-288-292-19321
; Sequence 19321, Application US/60288292
; GENERAL INFORMATION:
;  APPLICANT: Glenn, Matthew
;  APPLICANT:  Norriss, Michael G
;  TITLE OF INVENTION: Compounds isolated from forage plants
;  TITLE OF INVENTION:  and methods for their use.
;  FILE REFERENCE: 1058P
;  CURRENT APPLICATION NUMBER: US/60/288,292
;  CURRENT FILING DATE:  2001-05-02
;  NUMBER OF SEQ ID NOS: 49762
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 19321
;   LENGTH: 45
;   TYPE: DNA
;   ORGANISM: Festuca arundinaceae
US-60-288-292-19321

  Query Match             0.7%;  Score 22.2;  DB 11;  Length 45;
  Best Local Similarity   69.8%;  Pred. No. 7.1e+04;
  Matches   30;  Conservative    0;  Mismatches   13;  Indels    0;  Gaps    0;

Qy   1520 TCATCCATAGAGACATGAAATCCAACAATATATTTCTCCATGA 1562
          ||  ||| .|||| || ||||||| | | ||| | |||  |||
Db      3 TCGCCCACCGAGATATTAAATCCAGCCACATAATGCTCTTTGA 45


RESULT 10
US-10-293-338-4068
; Sequence 4068, Application US/10293338
; GENERAL INFORMATION:
;  APPLICANT: RosettaGenomics LTD
;  TITLE OF INVENTION: BIOINFORMATICALLY DETECTABLE GROUP OF NOVEL REGULATORY GENES F
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: 45282
;  CURRENT APPLICATION NUMBER: US/10/293,338
;  CURRENT FILING DATE:  2002-11-14
;  NUMBER OF SEQ ID NOS: 8785
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4068
;   LENGTH: 22
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-293-338-4068

  Query Match             0.7%;  Score 22;  DB 9;  Length 22;
  Best Local Similarity   100.0%;  Pred. No. 5.7e+04;
  Matches   22;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy    988 TCAGCCTCACCTTCAGCCCTGT 1009
          ||||||||||||||||||||||
Db      1 TCAGCCTCACCTTCAGCCCTGT 22


RESULT 11
US-10-349-143-3876
; Sequence 3876, Application US/10349143
; GENERAL INFORMATION:
;  APPLICANT: Cohen, Daniel
;  APPLICANT:  Blumenfeld, Marta
;  APPLICANT:  Chumakov, Ilya
;  TITLE OF INVENTION: Biallelic markers for use in constructing a high density...
;  FILE REFERENCE: GENSET.020CP1
;  CURRENT APPLICATION NUMBER: US/10/349,143
;  CURRENT FILING DATE:  2003-01-21
;  PRIOR APPLICATION NUMBER: US/09/422,978
;  PRIOR FILING DATE: 1999-10-20
;  PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 09/298,850
;  PRIOR FILING DATE: EARLIER FILING DATE: 1999-04-21
;  PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/109,732
;  PRIOR FILING DATE: EARLIER FILING DATE: 1998-11-23
;  PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/082,614
;  PRIOR FILING DATE: EARLIER FILING DATE: 1998-04-21
;  NUMBER OF SEQ ID NOS: 11796
; SEQ ID NO 3876
;   LENGTH: 47
;   TYPE: DNA
;   ORGANISM: Homo Sapiens
;   FEATURE:
;   NAME/KEY: allele
;   LOCATION: 24
;   OTHER INFORMATION: 99-4254-307 : polymorphic base A or G
US-10-349-143-3876

  Query Match             0.7%;  Score 22;  DB 9;  Length 47;
  Best Local Similarity   67.4%;  Pred. No. 8.3e+04;
  Matches   31;  Conservative    0;  Mismatches   15;  Indels    0;  Gaps    0;

Qy   2554 AACAGCCCAGGACTGCCGAGACTCTGGCCGCCCGAAGGAGCCTGCT 2599
          |||||||  || ||  ||  ||    ||  ||| |||||||||| ||
Db      1 AACAGCCTTGGGCTCACGTTACARCAGCATCCCCAAGGAGCCTCCT 46


RESULT 12
PCT-US02-14877A-875
; Sequence 875, Application PC/TUS0214877A
; GENERAL INFORMATION:
```

```
;  APPLICANT: Genome Therapeutics Corporation and
;  APPLICANT:  Allen, Kristina M.
;  APPLICANT:  Yaworsky, Paul
;  APPLICANT:  Morales, Arturo J.
;  APPLICANT:  Graham, James R.
;  APPLICANT:  Anisowicz, Anthony
;  APPLICANT:  Liu, Wei
;  TITLE OF INVENTION: HBM Variants that Modulate Bone Mass and Lipid Levels
;  FILE REFERENCE: 032796-135
;  CURRENT APPLICATION NUMBER: PCT/US02/14877A
;  CURRENT FILING DATE:  2002-05-13
;  PRIOR APPLICATION NUMBER: US 60/290,071
;  PRIOR FILING DATE: 2001-05-11
;  PRIOR APPLICATION NUMBER: US 60/291,311
;  PRIOR FILING DATE: 2001-05-17
;  PRIOR APPLICATION NUMBER: US 60/353,058
;  PRIOR FILING DATE: 2002-02-01
;  PRIOR APPLICATION NUMBER: US 60/361,293
;  PRIOR FILING DATE: 2002-03-04
;  NUMBER OF SEQ ID NOS: 1086
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 875
;   LENGTH: 25
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: primer
PCT-US02-14877A-875

  Query Match             0.7%;  Score 21.8;  DB 1;  Length 25;
  Best Local Similarity   92.0%;  Pred. No. 7e+04;
  Matches   23;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy    2796 TCTCTAACAAACAAACAAACAAACA 2820
           |||| |||||||||||||||||| |
Db       1 TCTCAAACAAACAAACAAACAAAAA 25


RESULT 13
US-60-427-808-320640
; Sequence 320640, Application US/60427808
; GENERAL INFORMATION:
;  APPLICANT: Xue Mei Zhou
;  TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
;  FILE REFERENCE: 3528
;  CURRENT APPLICATION NUMBER: US/60/427,808
;  CURRENT FILING DATE:  2002-11-20
;  NUMBER OF SEQ ID NOS: 982914
;  SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 320640
;   LENGTH: 25
;   TYPE: DNA
;   ORGANISM: Mus musculus
US-60-427-808-320640

  Query Match             0.7%;  Score 21.8;  DB 11;  Length 25;
  Best Local Similarity   92.0%;  Pred. No. 7e+04;
  Matches   23;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy    2210 CAGGGCCTTAACTTCATGTTGCCTT 2234
           |||||||||||| |||| |||||||
Db       1 CAGGGCCTTAACATCATATTGCCTT 25


RESULT 14
US-60-427-808-556622
; Sequence 556622, Application US/60427808
; GENERAL INFORMATION:
;  APPLICANT: Xue Mei Zhou
;  TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
;  FILE REFERENCE: 3528
;  CURRENT APPLICATION NUMBER: US/60/427,808
;  CURRENT FILING DATE:  2002-11-20
;  NUMBER OF SEQ ID NOS: 982914
;  SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 556622
;   LENGTH: 25
;   TYPE: DNA
;   ORGANISM: Mus musculus
US-60-427-808-556622

  Query Match             0.7%;  Score 21.8;  DB 11;  Length 25;
  Best Local Similarity   92.0%;  Pred. No. 7e+04;
  Matches   23;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy    2214 GCCTTAACTTCATGTTGCCTTCTTT 2238
           |||||||||||| ||||||||||
Db       1 GCCTTAACTTCAAATTGCCTTCTTT 25


RESULT 15
US-60-427-808-917221
; Sequence 917221, Application US/60427808
; GENERAL INFORMATION:
;  APPLICANT: Xue Mei Zhou
;  TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
;  FILE REFERENCE: 3528
;  CURRENT APPLICATION NUMBER: US/60/427,808
;  CURRENT FILING DATE:  2002-11-20
;  NUMBER OF SEQ ID NOS: 982914
;  SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 917221
;   LENGTH: 25
;   TYPE: DNA
;   ORGANISM: Mus musculus
US-60-427-808-917221

  Query Match             0.7%;  Score 21.8;  DB 11;  Length 25;
  Best Local Similarity   92.0%;  Pred. No. 7e+04;
  Matches   23;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy    2217 TTAACTTCATGTTGCCTTCTTTTCT 2241
           |||||||||| | ||||||||||||
Db       1 TTAACTTCATATAGCCTTCTTTTCT 25


Search completed: May 16, 2003, 12:41:39
Job time : 1374 secs
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OM nucleic - nucleic search, using sw model

Run on: May 16, 2003, 05:51:03 ; Search time 4039 Seconds
(without alignments)
11937.104 Million cell updates/sec

Title: US-10-057-550A-64
Perfect score: 2977
Sequence: 1 ccgaatgtgaccgcctcccg.....taataaaataaattaaattt 2977

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 16154066 seqs, 8097743376 residues

Total number of hits satisfying chosen parameters: 102860

Minimum DB seq length: 0
Maximum DB seq length: 50

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : EST:*
1: em_estba:*
2: em_esthum:*
3: em_estin:*
4: em_estmu:*
5: em_estov:*
6: em_estpl:*
7: em_estro:*
8: em_htc:*
9: gb_est1:*
10: gb_est2:*
11: gb_htc:*
12: gb_est3:*
13: gb_est4:*
14: gb_est5:*
15: em_estfun:*
16: em_estom:*
17: gb_gss:*
18: em_gss_hum:*
19: em_gss_inv:*
20: em_gss_pln:*
21: em_gss_vrt:*
22: em_gss_fun:*
23: em_gss_mam:*
24: em_gss_mus:*
25: em_gss_other:*
26: em_gss_pro:*
27: em_gss_rod:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	40.8	1.4	48	14	H26959	H26959 yo58c08.s1
c 2	24.6	0.8	47	17	AZ425831	AZ425831 1M0206D14
c 3	22.8	0.8	45	2	HSM002199	A1037866 Homo sapi
4	22	0.7	40	17	AZ391073	AZ391073 1M0152I24
5	22	0.7	43	12	BE969098	BE969098 601650077
c 6	21.8	0.7	47	13	BJ047667	BJ047667 BJ047667
c 7	21.8	0.7	49	9	AI316598	AI316598 uk62a04.y
c 8	21.8	0.7	49	17	AZ593107	AZ593107 1M0404O22
9	21.6	0.7	45	2	HSM003616	A1039140 Homo sapi
c 10	21.4	0.7	50	9	AU270282	AU270282 AU270282
11	21	0.7	43	17	AZ310534	AZ310534 1M0025J03
12	21	0.7	44	9	AL587842	AL587842 AL587842
c 13	20.8	0.7	36	17	AZ512567	AZ512567 1M0358G17
14	20.8	0.7	44	2	HSM001110	A1036793 Homo sapi
c 15	20.8	0.7	45	17	AZ602556	AZ602556 1M0421E20
c 16	20.8	0.7	49	9	AI267816	AI267816 aq35c09.x
c 17	20.8	0.7	50	9	AU102743	AU102743 AU102743
c 18	20.8	0.7	50	12	BF013308	BF013308 rk29c02.y
19	20.6	0.7	46	9	AA737998	AA737998 nx15b01.s
20	20.6	0.7	46	9	AI360975	AI360975 qy02f12.x
c 21	20.6	0.7	50	9	AI708455	AI708455 as97e06.x
c 22	20.4	0.7	36	17	AZ774766	AZ774766 2M0004G05
23	20.4	0.7	40	9	AL048749	AL048749 DKFZp566K
24	20.4	0.7	46	9	AI439612	AI439612 tc91b01.x
25	20.4	0.7	48	17	DR15D19T	AL748117 Danio rer
c 26	20.4	0.7	49	9	AI173140	AI173140 vz78c03.r
27	20.4	0.7	50	9	AU104895	AU104895 AU104895
c 28	20.4	0.7	50	17	AZ347604	AZ347604 1M0083G13
29	20.2	0.7	36	14	T57700	T57700 yc01d11.s1
30	20.2	0.7	49	17	AZ803783	AZ803783 2M0064B22
c 31	20.2	0.7	50	9	AA139046	AA139046 mn48c12.r
c 32	20.2	0.7	50	14	BQ258029	BQ258029 NISC_kp08
33	20	0.7	37	10	AW334659	AW334659 S38H4 AGS
c 34	20	0.7	39	13	BJ065085	BJ065085 BJ065085
c 35	20	0.7	40	17	BH796875	BH796875 1008077F0
c 36	20	0.7	41	17	AZ793496	AZ793496 2M0046I16
c 37	20	0.7	43	9	AI608816	AI608816 tw21g04.x
c 38	20	0.7	46	17	AZ806877	AZ806877 2M0069A14
c 39	20	0.7	49	9	AA388129	AA388129 vc86f05.r
40	20	0.7	50	9	AA853120	AA853120 NHTBCae03
41	20	0.7	50	9	AJ499559	AJ499559 AJ499559
42	20	0.7	50	9	AU104458	AU104458 AU104458
43	20	0.7	50	9	AU104922	AU104922 AU104922
44	20	0.7	50	9	AA564185	AA564185 nj04d11.s
c 45	20	0.7	50	13	BI496942	BI496942 df129g10.

ALIGNMENTS

RESULT 1
H26959
LOCUS H26959 48 bp mRNA linear EST 16-AUG-1995
DEFINITION yo58c08.s1 Soares breast 3NbHBst Homo sapiens cDNA clone IMAGE:182126 3' similar to gb:X06409 RAF PROTO-ONCOGENE SERINE/THREONINE-PROTEIN KINASE (HUMAN);, mRNA sequence.
ACCESSION H26959
VERSION H26959.1 GI:896949
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 48)
AUTHORS Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M., Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M., Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F., Trevaskis,E., Waterston,R., Williamson,A., Wohldmann,P. and Wilson,R.
TITLE The WashU-Merck EST Project
JOURNAL Unpublished (1995)
COMMENT Contact: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
Insert Size: 603
High quality sequence starts: 1
High quality sequence stops: 1

```
            Source: IMAGE Consortium, LLNL
            This clone is available royalty-free through LLNL ; contact the
            IMAGE Consortium (info@image.llnl.gov) for further information.
            Trace considered overall poor quality
            Insert Length: 603    Std Error: 0.00
            Seq primer: Promega -21m13
            High quality sequence stop: 1.
FEATURES              Location/Qualifiers
     source           1. .48
                      /organism="Homo sapiens"
                      /db_xref="GDB:3815326"
                      /db_xref="taxon:9606"
                      /clone="IMAGE:182126"
                      /clone_lib="Soares breast 3NbHBst"
                      /sex="Female"
                      /dev_stage="adult"
                      /lab_host="DH10B (ampicillin resistant)"
                      /note="Organ: breast; Vector: pT7T3D (Pharmacia) with a
                      modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st
                      strand cDNA was primed with a Not I - oligo(dT) primer [5'
                      TGTTACCAATCTGAAGTGGGAGCGGCCGCCCTTTTTTTTTTTTTTTTT 3'],
                      double-stranded cDNA was ligated to Eco RI adaptors
                      (Pharmacia), digested with Not I and cloned into the Not I
                      and Eco RI sites of a modified pT7T3 vector (Pharmacia).
                      Library went through one round of normalization to a Cot =
                      20. Library constructed by Bento Soares and M.Fatima
                      Bonaldo."
BASE COUNT       12 a      6 c      9 g     17 t      4 others
ORIGIN

  Query Match              1.4%;  Score 40.8;  DB 14;  Length 48;
  Best Local Similarity   87.5%;  Pred. No. 7.8;
  Matches   42;  Conservative    0;  Mismatches    6;  Indels    0;  Gaps    0;

Qy   2885 TTTGGGTTTTAATTTTGTTTTTATTGCACCTGACAAAATACAGTTATC 2932
           ||||||||| ||||  ||||| || ||||| ||||||||||||||||
Db      1 TTTGGGTTTNAATTNNGTTTTNATGGCACCGGACAAAATACAGTTATC 48


RESULT 2
AZ425831/c
LOCUS       AZ425831                 47 bp    DNA     linear   GSS 03-OCT-2000
DEFINITION  1M0206D14F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
            clone UUGC1M0206D14 F, DNA sequence.
ACCESSION   AZ425831
VERSION     AZ425831.1  GI:10549940
KEYWORDS    GSS.
SOURCE      house mouse.
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 47)
  AUTHORS   Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
            Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly
            ,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.
            and Wright,D.,Weiss,R.
  TITLE     Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Robert B. Weiss
            University of Utah Genome Center
            University of Utah
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
            84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177
            Email: ddunn@genetics.utah.edu
            Insert Length: 10000    Std Error: 0.00
            Plate: 0206  row: D  column: 14
            Seq primer: CGTTGTAAAACGACGGCCAGT
            Class: plasmid ends
            High quality sequence stop: 47.
FEATURES              Location/Qualifiers
     source           1. .47
                      /organism="Mus musculus"
                      /strain="C57BL/6J"
                      /db_xref="taxon:10090"
                      /clone="UUGC1M0206D14"
                      /clone_lib="Mouse 10kb plasmid UUGC1M library"
                      /sex="Male"
                      /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
                      /note="Vector: PWD42nv; Purified genomic DNA from M.
                      musculus C57BL/6J (male) was obtained  from the Jackson
                      Laboratory Mouse DNA Resource
                      (http://www.jax.org/resources/documents/dnares/). The DNA
                      was hydrodynamically sheared by repeated passage through a
                      0.005 inch orifice at constant velocity. The sheared DNA
                      was blunt end-repaired with T4 DNA polymerase and T4
                      polynucleotide kinase. Adaptor oligonucleotides were
                      ligated to the blunt ends in high  molar excess. The
                      adaptored DNA was purified and size-selected for a 9.5 to
                      10.5 kb range using preparative agarose gel
                      electrophoresis. Vector DNA was prepared from a derivative
                      of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
                      inducible derivative of plasmid R1. The vector was ligated
                      with adaptors complementary to the insert adaptors and
                      purified. The sheared, adaptored mouse DNA was annealed to
                      adaptored vector DNA, and transformed into
                      chemically-competent E. coli XL10-Gold (Stratagene) cells
                      and selected for ampicillin resistance."
BASE COUNT       6 a      5 c     12 g     24 t
ORIGIN

  Query Match              0.8%;  Score 24.6;  DB 17;  Length 47;
  Best Local Similarity   76.9%;  Pred. No. 1.8e+05;
  Matches   30;  Conservative    0;  Mismatches    9;  Indels    0;  Gaps    0;

Qy   2784 GGCCAGCCTGTTTCTCTAACAAACAAACAAACAAACAGC 2822
           | ||||  | |||    |||||||||||||||||||| |
Db     47 GCCCAGGTTATTTTCAGAACAAACAAACAAACAAACAAC 9


RESULT 3
HSM002199/c
ID   HSM002199  standard; RNA; EST; 45 BP.
XX
AC   AL037866;
XX
SV   AL037866.1
XX
DT   12-MAR-1999 (Rel. 59, Created)
DT   12-MAR-1999 (Rel. 59, Last updated, Version 1)
XX
DE   Homo sapiens mRNA; EST DKFZp564J147_r1  (from clone DKFZp564J147)
XX
KW   EST; expressed sequence tag.
XX
OS   Homo sapiens (human)
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia;
OC   Eutheria; Primates; Catarrhini; Hominidae; Homo.
XX
RN   [1]
RP   1-45
RA   Bloecker H., Boecher M., Brandt P., Mewes W., Gassenhuber J., Wiemann S.;
RT   ;
RL   Submitted (12-MAR-1999) to the EMBL/GenBank/DDBJ databases.
RL   MIPS, Am Klopferspitz 18a D-82152 Martinsried, GERMANY
XX
CC   Clone from S. Wiemann, sequenced by GBF within the cDNA
CC   sequencing consortium of the German Genome Project
CC   No s1 sequence available
CC   This clone is available at the RZPD in Berlin
CC   Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
CC   Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de
XX
FH   Key             Location/Qualifiers
```

```
FH
FT   source          1. .45
FT                   /db_xref="taxon:9606"
FT                   /organism="Homo sapiens"
FT                   /clone="DKFZp564J147"
FT                   /clone_lib="564 (synonym: hfbr2). Vector pAMP1; host
FT                   Xl-2blue; sites NotI + SalI"
FT                   /dev_stage="fetal"
FT                   /tissue_type="brain"
XX
SQ   Sequence 45 BP; 38 A; 1 C; 5 G; 1 T; 0 other;

  Query Match             0.8%;  Score 22.8;  DB 2;  Length 45;
  Best Local Similarity   71.4%;  Pred. No. 5.4e+05;
  Matches   30;  Conservative    0;  Mismatches   12;  Indels    0;  Gaps    0;

Qy    2873 TTTTCTTGATGATTTGGGTTTTAATTTTGTTTTTATTGCACC 2914
           |||| ||  |  |||   ||||  |||| ||||| |||||||
Db      43 TTTTTTTTTTTTTTTTTCTTTTTTTTTTTTTTTTTTGCACC 2

RESULT 4
AZ391073
LOCUS       AZ391073                 40 bp    DNA     linear   GSS 03-OCT-2000
DEFINITION  1M0152I24R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
            clone UUGC1M0152I24 R, DNA sequence.
ACCESSION   AZ391073
VERSION     AZ391073.1  GI:10506116
KEYWORDS    GSS.
SOURCE      house mouse.
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 40)
  AUTHORS   Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
            Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly
            ,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.
            and Wright,D.,Weiss,R.
  TITLE     Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Robert B. Weiss
            University of Utah Genome Center
            University of Utah
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
            84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177
            Email: ddunn@genetics.utah.edu
            Insert Length: 10000   Std Error: 0.00
            Plate: 0152  row: I  column: 24
            Seq primer: CACACAGGAAACAGCTATGACC
            Class: plasmid ends
            High quality sequence stop: 40.
FEATURES             Location/Qualifiers
     source          1. .40
                     /organism="Mus musculus"
                     /strain="C57BL/6J"
                     /db_xref="taxon:10090"
                     /clone="UUGC1M0152I24"
                     /clone_lib="Mouse 10kb plasmid UUGC1M library"
                     /sex="Male"
                     /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
                     /note="Vector: PWD42nv; Purified genomic DNA from M.
                     musculus C57BL/6J (male) was obtained from the Jackson
                     Laboratory Mouse DNA Resource
                     (http://www.jax.org/resources/documents/dnares/). The DNA
                     was hydrodynamically sheared by repeated passage through a
                     0.005 inch orifice at constant velocity. The sheared DNA
                     was blunt end-repaired with T4 DNA polymerase and T4
                     polynucleotide kinase. Adaptor oligonucleotides were
                     ligated to the blunt ends in high molar excess. The
                     adaptored DNA was purified and size-selected for a 9.5 to
                     10.5 kb range using preparative agarose gel
                     electrophoresis. Vector DNA was prepared from a derivative
                     of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
                     inducible derivative of plasmid R1. The vector was ligated
                     with adaptors complementary to the insert adaptors and
                     purified. The sheared, adaptored mouse DNA was annealed to
                     adaptored vector DNA, and transformed into
                     chemically-competent E. coli XL10-Gold (Stratagene) cells
                     and selected for ampicillin resistance."
BASE COUNT        0 a      0 c      8 g     32 t
ORIGIN

  Query Match             0.7%;  Score 22;  DB 17;  Length 40;
  Best Local Similarity   73.7%;  Pred. No. 8.6e+05;
  Matches   28;  Conservative    0;  Mismatches   10;  Indels    0;  Gaps    0;

Qy    2872 GTTTTCTTGATGATTTGGGTTTTAATTTTGTTTTTATT 2909
           ||||  ||| |  ||| | ||||  |||||||||| ||
Db       1 GTTTGTTTGTTTGTTTTGTTTTTGTTTTGTTTTTGTT 38

RESULT 5
BE969098
LOCUS       BE969098                 43 bp    mRNA    linear   EST 04-OCT-2000
DEFINITION  601650077R1 NIH_MGC_74 Homo sapiens cDNA clone IMAGE:3933811 3',
            mRNA sequence.
ACCESSION   BE969098
VERSION     BE969098.1  GI:10581742
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 43)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: CLONETECH Laboratories, Inc.
            cDNA Library Preparation: CLONETECH Laboratories, Inc.
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: Incyte Genomics, Inc.
            Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLCM773  row: j  column: 20.
FEATURES             Location/Qualifiers
     source          1. .43
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:3933811"
                     /clone_lib="NIH_MGC_74"
                     /lab_host="DH10B (T1 phage-resistant)"
                     /note="Organ: heart; Vector: pDNR-LIB (Clontech); Site_1:
                     : SfiI (ggccgcctcggcc); Site_2: SfiI (ggccattatggcc); 5'
                     and 3' adaptors were used in cloning as follows: 5'
                     adaptor sequence: 5'-CACGGCCATTATGGCC-3' and 3' adaptor
                     sequence: 5'-ATTCTAGAGGCCGAGGCGGCCGACATG-dT(30)BN-3'
                     (where B = A, C, or G and N = A, C, G, or T). Average
                     insert size 1.25 kb (range 0.6-4.0 kb). 14/15 colonies
                     contained inserts by PCR. This library was enriched for
                     full-length clones and was constructed by Clontech
                     Laboratories (Palo Alto, CA)."
BASE COUNT        0 a      1 c      4 g     38 t
ORIGIN

  Query Match             0.7%;  Score 22;  DB 12;  Length 43;
  Best Local Similarity   73.7%;  Pred. No. 8.7e+05;
  Matches   28;  Conservative    0;  Mismatches   10;  Indels    0;  Gaps    0;

Qy    2872 GTTTTCTTGATGATTTGGGTTTTAATTTTGTTTTTATT 2909
           ||||| ||  |  ||| |||||  |||||||||| ||
```

```
Db      2 GTTTTGTTTTTTTTTTTTGTTTTTCTTTTGTTTTTTTT 39


RESULT 6
BJ047667/c
LOCUS       BJ047667                 47 bp    mRNA    linear   EST 05-DEC-2001
DEFINITION  BJ047667 NIBB Mochii normalized Xenopus neurula library Xenopus
            laevis cDNA clone XL017e20 3', mRNA sequence.
ACCESSION   BJ047667
VERSION     BJ047667.1  GI:17374496
KEYWORDS    EST.
SOURCE      African clawed frog.
  ORGANISM  Xenopus laevis
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
            Xenopodinae; Xenopus.
REFERENCE   1  (bases 1 to 47)
  AUTHORS   Kitayama,A., Terasaka,C., Mochii,M., Ueno,N., Shin-i,T. and Kohara
            ,Y.
  TITLE     Expressed genes in X. laevis embryo
  JOURNAL   Unpublished (2001)
COMMENT     Contact: Tadasu Shin-i
            Center For Genetic Resource Information
            National Institute of Genetics
            1111 Yata, Mishima, Shizuoka 411-8540, Japan
            Tel: 81-559-81-6856
            Fax: 81-559-81-6855
            Email: tshini@genes.nig.ac.jp.
FEATURES             Location/Qualifiers
     source          1. .47
                     /organism="Xenopus laevis"
                     /db_xref="taxon:8355"
                     /clone="XL017e20"
                     /clone_lib="NIBB Mochii normalized Xenopus neurula
                     library"
                     /tissue_type="whole embryo"
                     /dev_stage="stage 15"
                     /note="Vector: pBSRN3; Site_1: NotI; Site_2: EcoRI; cDNAs
                     were oligo-dT primed and directionally cloned. Staging
                     according to  Nieuwkoop and Faber. Library is subtracted
                     and was constructed by N. Garrett  and A.M. Zorn,
                     (Wellcome/CRC Institute). "
BASE COUNT       35 a      4 c      3 g      3 t      2 others
ORIGIN

  Query Match             0.7%;  Score 21.8;  DB 13;  Length 47;
  Best Local Similarity   67.4%;  Pred. No. 1e+06;
  Matches   29;  Conservative    0;  Mismatches   14;  Indels    0;  Gaps    0;

Qy   2871 GGTTTTCTTGATGATTTGGGTTTTAATTTTGTTTTTATTGCAC 2913
           | |||| ||  || ||| . ||||  |||| ||||| ||  ||
Db     45 GTTTTTTTTTTTGTTTTTNNTTTTTTTTTTTTTTTTTTTCAAC 3


RESULT 7
AI316598/c
LOCUS       AI316598                 49 bp    mRNA    linear   EST 17-DEC-1998
DEFINITION  uk62a04.y1 Schiller mouse MAC16 Mus musculus cDNA clone
            IMAGE:1973550 5', mRNA sequence.
ACCESSION   AI316598
VERSION     AI316598.1  GI:4031865
KEYWORDS    EST.
SOURCE      house mouse.
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 49)
  AUTHORS   Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.,
            Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,
            Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,
            Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
            Waterston,R.
  TITLE     The WashU-HHMI Mouse EST Project
  JOURNAL   Unpublished (1996)
COMMENT     Contact: Marra M/Mouse EST Project
            WashU-HHMI Mouse EST Project
            Washington University School of MedicineP
            4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
            Tel: 314 286 1800
            Fax: 314 286 1810
            Email: mouseest@watson.wustl.edu
            This clone is available royalty-free through LLNL ; contact the
            IMAGE Consortium (info@image.llnl.gov) for further information.
            MGI:990290
            Seq primer: -40RP from Gibco.
FEATURES             Location/Qualifiers
     source          1. .49
                     /organism="Mus musculus"
                     /db_xref="taxon:10090"
                     /clone="IMAGE:1973550"
                     /clone_lib="Schiller mouse MAC16"
                     /cell_line="colon cancer cell line"
                     /lab_host="SOLR"
                     /note="Vector: pBluescript SK- (Stratagene); Site_1: EcoRI
                     ; Site_2: XhoI; Double-stranded cDNA was prepared from
                     cell line MAC16 using primer
                     5'-GAGAGAGAGAGAGAGAGAAACTAGTCTGAGT(18)-3'.  An EcoRI
                     adaptor was used on the 5' end of the cDNA as follows:
                     5'-AATTCGGCACGAG-3'.  The library was size-selected and
                     went through one round of amplification.  Average insert
                     size is 1.7 kb, with a range from 0.4-12 kb.  This library
                     was constructed by Dr. Martin Schiller (Johns Hopkins
                     University). "
BASE COUNT       40 a      4 c      4 g      1 t
ORIGIN

  Query Match             0.7%;  Score 21.8;  DB 9;  Length 49;
  Best Local Similarity   65.3%;  Pred. No. 1e+06;
  Matches   32;  Conservative    0;  Mismatches   17;  Indels    0;  Gaps    0;

Qy   2872 GTTTTCTTGATGATTTGGGTTTTAATTTTGTTTTTATTGCACCTGACAA 2920
           ||||| ||  |  |||   ||||  |||| ||||| || | | || | |
Db     49 GTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTCTCGTGCCGA 1


RESULT 8
AZ593107/c
LOCUS       AZ593107                 49 bp    DNA     linear   GSS 13-DEC-2000
DEFINITION  1M0404022F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
            clone UUGC1M0404022 F, DNA sequence.
ACCESSION   AZ593107
VERSION     AZ593107.1  GI:11715297
KEYWORDS    GSS.
SOURCE      house mouse.
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 49)
  AUTHORS   Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
            Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly
            ,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.
            and Wright,D.,Weiss,R.
  TITLE     Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Robert B. Weiss
            University of Utah Genome Center
            University of Utah
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
            84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177
            Email: ddunn@genetics.utah.edu
            Insert Length: 10000   Std Error: 0.00
            Plate: 0404  row: O  column: 22
            Seq primer: CGTTGTAAAACGACGGCCAGT
```

```
          Class: plasmid ends
          High quality sequence stop: 49.
FEATURES             Location/Qualifiers
     source          1. .49
                     /organism="Mus musculus"
                     /strain="C57BL/6J"
                     /db_xref="taxon:10090"
                     /clone="UUGC1M0404022"
                     /clone_lib="Mouse 10kb plasmid UUGC1M library"
                     /sex="Male"
                     /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
                     /note="Vector: PWD42nv; Purified genomic DNA from M.
                     musculus C57BL/6J (male) was obtained from the Jackson
                     Laboratory Mouse DNA Resource
                     (http://www.jax.org/resources/documents/dnares/). The DNA
                     was hydrodynamically sheared by repeated passage through a
                     0.005 inch orifice at constant velocity. The sheared DNA
                     was blunt end-repaired with T4 DNA polymerase and T4
                     polynucleotide kinase. Adaptor oligonucleotides were
                     ligated to the blunt ends in high molar excess. The
                     adaptored DNA was purified and size-selected for a 9.5 to
                     10.5 kb range using preparative agarose gel
                     electrophoresis. Vector DNA was prepared from a derivative
                     of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
                     inducible derivative of plasmid R1. The vector was ligated
                     with adaptors complementary to the insert adaptors and
                     purified. The sheared, adaptored mouse DNA was annealed to
                     adaptored vector DNA, and transformed into
                     chemically-competent E. coli XL10-Gold (Stratagene) cells
                     and selected for ampicillin resistance."
BASE COUNT       12 a      8 c      11 g      18 t
ORIGIN

  Query Match             0.7%;  Score 21.8;  DB 17;  Length 49;
  Best Local Similarity   65.3%;  Pred. No. 1e+06;
  Matches   32;  Conservative    0;  Mismatches   17;  Indels    0;  Gaps    0;

Qy    2803 CAAACAAACAAACAAACAGCCTTGTTTCTCTAGTCACATCATGTGTATA 2851
           || ||| ||| ||| ||||  || |   |  ||| |  | |||||||  |
Db      49 CACACACACACACACACAGAGTTTTGCATGAAGTTATGTAATGTGTACA 1


RESULT 9
HSM003616
ID   HSM003616  standard; RNA; EST; 45 BP.
XX
AC   AL039140;
XX
SV   AL039140.1
XX
DT   12-MAR-1999 (Rel. 59, Created)
DT   12-MAR-1999 (Rel. 59, Last updated, Version 1)
XX
DE   Homo sapiens mRNA; EST DKFZp566L194_r1  (from clone DKFZp566L194)
XX
KW   EST; expressed sequence tag.
XX
OS   Homo sapiens (human)
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia;
OC   Eutheria; Primates; Catarrhini; Hominidae; Homo.
XX
RN   [1]
RP   1-45
RA   Bloecker H., Boecher M., Brandt P., Mewes W., Gassenhuber J., Wiemann S.;
RT   ;
RL   Submitted (12-MAR-1999) to the EMBL/GenBank/DDBJ databases.
RL   MIPS, Am Klopferspitz 18a D-82152 Martinsried, GERMANY
XX
CC   Clone from S. Wiemann, sequenced by GBF within the cDNA
CC   sequencing consortium of the German Genome Project
CC   No s1 sequence available
CC   This clone is available at the RZPD in Berlin
CC   Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
CC   Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de
XX
FH   Key             Location/Qualifiers
FH
FT   source          1. .45
FT                   /db_xref="taxon:9606"
FT                   /organism="Homo sapiens"
FT                   /clone="DKFZp566L194"
FT                   /clone_lib="566 (synonym: hfkd2). Vector pAMP1; host
FT                   Xl-2blue; sites NotI + SalI"
FT                   /dev_stage="fetal"
FT                   /tissue_type="kidney"
XX
SQ   Sequence 45 BP; 24 A; 6 C; 8 G; 7 T; 0 other;

  Query Match             0.7%;  Score 21.6;  DB 2;  Length 45;
  Best Local Similarity   68.2%;  Pred. No. 1.1e+06;
  Matches   30;  Conservative    0;  Mismatches   14;  Indels    0;  Gaps    0;

Qy    2775 GGGCCGCAGGGCCAGCCTGTTTCTCTAACAAACAAACAAACAAA 2818
           ||||   ||    || || | ||||||| ||| ||| ||| |||
Db       2 GGGCAATAGACTGAGACTCTGTCTCTAAAAAAAAAAAAAAAAA 45


RESULT 10
AU270282/c
LOCUS       AU270282                 50 bp    mRNA    linear   EST 10-MAY-2002
DEFINITION  AU270282 VS Dictyostelium discoideum cDNA clone VSJ664 3', mRNA
            sequence.
ACCESSION   AU270282
VERSION     AU270282.1  GI:20529080
KEYWORDS    EST.
SOURCE      Dictyostelium discoideum.
  ORGANISM  Dictyostelium discoideum
            Eukaryota; Mycetozoa; Dictyosteliida; Dictyostelium.
REFERENCE   1  (bases 1 to 50)
  AUTHORS   Urushihara,H., Morio,T., Saito,T., Koriki,E., Ochiai,H., Maeda,M.,
            Takeuchi,I., Kohara,Y. and Tanaka,Y.
  TITLE     Population analysis of cDNAs from unicellular and multicellular
            stages of Dictyostelium discoideum
  JOURNAL   Unpublished (2002)
COMMENT     Contact: Hideko Urushihara
            Institute of Biological Sciences
            University of Tsukuba
            1-1-1 Tennoudai, Tsukuba, Ibaraki 305-8572, Japan
            Tel: 81-298-53-4664
            Fax: 81-298-53-6614
            Email: hideko@biol.tsukuba.ac.jp.
FEATURES             Location/Qualifiers
     source          1. .50
                     /organism="Dictyostelium discoideum"
                     /strain="AX4"
                     /db_xref="taxon:44689"
                     /clone="VSJ664"
                     /clone_lib="VS"
                     /sex="mat A"
                     /dev_stage="vegetative"
BASE COUNT       36 a      3 c      1 g      4 t      6 others
ORIGIN

  Query Match             0.7%;  Score 21.4;  DB 9;  Length 50;
  Best Local Similarity   67.6%;  Pred. No. 1.3e+06;
  Matches   25;  Conservative    0;  Mismatches   12;  Indels    0;  Gaps    0;

Qy    2873 TTTTCTTGATGATTTGGGTTTTAATTTTGTTTTTATT 2909
           |||| || || | | ||||| |  ||   ||||| ||
Db      41 TTTTTTTTATTACTNGGGTTNTTNTTNNTTTTTTNTT 5


RESULT 11
AZ310534
LOCUS       AZ310534                 43 bp    DNA     linear   GSS 29-SEP-2000
DEFINITION  1M0025J03R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
```

```
            clone UUGC1M0025J03 R, DNA sequence.
ACCESSION   AZ310534
VERSION     AZ310534.1  GI:10352617
KEYWORDS    GSS.
SOURCE      house mouse.
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 43)
  AUTHORS   Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
            Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly
            ,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.
            and Wright,D.,Weiss,R.
  TITLE     Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Robert B. Weiss
            University of Utah Genome Center
            University of Utah
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
            84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177
            Email: ddunn@genetics.utah.edu
            Insert Length: 10000   Std Error: 0.00
            Plate: 0025  row: J  column: 03
            Seq primer: CACACAGGAAACAGCTATGACC
            Class: plasmid ends
            High quality sequence stop: 43.
FEATURES             Location/Qualifiers
     source          1. .43
                     /organism="Mus musculus"
                     /strain="C57BL/6J"
                     /db_xref="taxon:10090"
                     /clone="UUGC1M0025J03"
                     /clone_lib="Mouse 10kb plasmid UUGC1M library"
                     /sex="Male"
                     /lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
                     /note="Vector: PWD42nv; Purified genomic DNA from M.
                     musculus C57BL/6J (male) was obtained  from the Jackson
                     Laboratory Mouse DNA Resource
                     (http://www.jax.org/resources/documents/dnares/). The DNA
                     was hydrodynamically sheared by repeated passage through a
                     0.005 inch orifice at constant velocity. The sheared DNA
                     was blunt end-repaired with T4 DNA polymerase and T4
                     polynucleotide kinase. Adaptor oligonucleotides were
                     ligated to the blunt ends in high  molar excess. The
                     adaptored DNA was purified and size-selected for a 9.5 to
                     10.5 kb range using preparative agarose gel
                     electrophoresis. Vector DNA was prepared from a derivative
                     of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
                     inducible derivative of plasmid R1. The vector was ligated
                     with adaptors complementary to the insert adaptors and
                     purified. The sheared, adaptored mouse DNA was annealed to
                     adaptored vector DNA, and transformed into
                     chemically-competent E. coli XL10-Gold (Stratagene) cells
                     and selected for ampicillin resistance."
BASE COUNT       26 a      10 c       4 g       3 t
ORIGIN

  Query Match             0.7%;  Score 21;  DB 17;  Length 43;
  Best Local Similarity   100.0%;  Pred. No. 1.6e+06;
  Matches   21;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy    2801 AACAAACAAACAAACAAACAG 2821
           |||||||||||||||||||||
Db       5 AACAAACAAACAAACAAACAG 25


RESULT 12
AL587842
LOCUS       AL587842                 44 bp    mRNA    linear   EST 02-MAR-2001
DEFINITION  AL587842 BP Chicken Brain Library Gallus gallus cDNA clone
            ROS064C05, mRNA sequence.
ACCESSION   AL587842
VERSION     AL587842.1  GI:13192876
KEYWORDS    EST.
SOURCE      chicken.
  ORGANISM  Gallus gallus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
            Phasianinae; Gallus.
REFERENCE   1  (bases 1 to 44)
  AUTHORS   Murray,F.
  TITLE     BP Chicken Brain Library
  JOURNAL   Unpublished (2001)
COMMENT     Contact: Frazer Murray
            Dept. Genomics and Bioinformatics
            Roslin Institute
            Roslin, Midlothian, EH25 9PS, UK
            Tel: +44 (0)131 527 4200
            Fax: +44 (0)131 440 0434
            Email: frazer.murray@bbsrc.ac.uk
            GCGGCCGCTTTTTTTTTTTTTTTTT 3' Poly A RNA purchased from Clonetech
            (*6854-
            Seq primer: M13F.
FEATURES             Location/Qualifiers
     source          1. .44
                     /organism="Gallus gallus"
                     /db_xref="taxon:9031"
                     /clone="ROS064C05"
                     /clone_lib="BP Chicken Brain Library"
                     /tissue_type="Brain"
                     /dev_stage="Unknown"
                     /lab_host="DH10B"
                     /note="Vector: pSPORT1; Site_1: Not1; Site_2: Sal1; Cloned
                     unidirectionally. Primer: Oligo dT. 5' adaptor sequence:
                     5' TCGACCTCGAG 3' ; 3' adaptor sequence: 5'
                     GCGGCCGCTTTTTTTTTTTTTTTTT 3' Poly A RNA purchased from
                     Clonetech (*6854-1)"
BASE COUNT       1 a       0 c       4 g      39 t
ORIGIN

  Query Match             0.7%;  Score 21;  DB 9;  Length 44;
  Best Local Similarity   73.0%;  Pred. No. 1.6e+06;
  Matches   27;  Conservative    0;  Mismatches   10;  Indels    0;  Gaps    0;

Qy    2873 TTTTCTTGATGATTTGGGTTTTAATTTTGTTTTTATT 2909
           |||| ||  |  ||| |||||| |||| ||||| ||
Db       4 TTTTTTTTTTTTTTTTGGTTTTTTTTTTTTTTTTTT 40


RESULT 13
AZ512567/c
LOCUS       AZ512567                 36 bp    DNA     linear   GSS 05-OCT-2000
DEFINITION  1M0358G17F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
            clone UUGC1M0358G17 F, DNA sequence.
ACCESSION   AZ512567
VERSION     AZ512567.1  GI:10693883
KEYWORDS    GSS.
SOURCE      house mouse.
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 36)
  AUTHORS   Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
            Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly
            ,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.
            and Wright,D.,Weiss,R.
  TITLE     Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Robert B. Weiss
            University of Utah Genome Center
            University of Utah
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
```

```
           84112, USA
           Tel: 801 585 5606
           Fax: 801 585 7177
           Email: ddunn@genetics.utah.edu
           Insert Length: 10000   Std Error: 0.00
           Plate: 0358  row: G  column: 17
           Seq primer: CGTTGTAAAACGACGGCCAGT
           Class: plasmid ends
           High quality sequence stop: 36.
FEATURES             Location/Qualifiers
     source          1. .36
                     /organism="Mus musculus"
                     /strain="C57BL/6J"
                     /db_xref="taxon:10090"
                     /clone="UUGC1M0358G17"
                     /clone_lib="Mouse 10kb plasmid UUGC1M library"
                     /sex="Male"
                     /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
                     /note="Vector: PWD42nv; Purified genomic DNA from M.
                     musculus C57BL/6J (male) was obtained  from the Jackson
                     Laboratory Mouse DNA Resource
                     (http://www.jax.org/resources/documents/dnares/). The DNA
                     was hydrodynamically sheared by repeated passage through a
                     0.005 inch orifice at constant velocity. The sheared DNA
                     was blunt end-repaired with T4 DNA polymerase and T4
                     polynucleotide kinase. Adaptor oligonucleotides were
                     ligated to the blunt ends in high  molar excess. The
                     adaptored DNA was purified and size-selected for a 9.5 to
                     10.5 kb range using preparative agarose gel
                     electrophoresis. Vector DNA was prepared from a derivative
                     of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
                     inducible derivative of plasmid R1. The vector was ligated
                     with adaptors complementary to the insert adaptors and
                     purified. The sheared, adaptored mouse DNA was annealed to
                     adaptored vector DNA, and transformed into
                     chemically-competent E. coli XL10-Gold (Stratagene) cells
                     and selected for ampicillin resistance."
BASE COUNT        0 a      0 c     15 g     21 t
ORIGIN

  Query Match             0.7%;  Score 20.8;  DB 17;  Length 36;
  Best Local Similarity   91.7%;  Pred. No. 1.8e+06;
  Matches   22;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy    2797 CTCTAACAAACAAACAAACAAACA 2820
           | | ||||||||||||||||||||
Db      30 CCCAAACAAACAAACAAACAAACA 7


RESULT 14
HSM001110
ID   HSM001110  standard; RNA; EST; 44 BP.
XX
AC   AL036793;
XX
SV   AL036793.1
XX
DT   12-MAR-1999 (Rel. 59, Created)
DT   12-MAR-1999 (Rel. 59, Last updated, Version 1)
XX
DE   Homo sapiens mRNA; EST DKFZp564K0763_r1  (from clone DKFZp564K0763)
XX
KW   EST; expressed sequence tag.
XX
OS   Homo sapiens (human)
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia;
OC   Eutheria; Primates; Catarrhini; Hominidae; Homo.
XX
RN   [1]
RP   1-44
RA   Duesterhoeft A., Lauber J., Mewes W., Gassenhuber J., Wiemann S.;
RT   ;
RL   Submitted (12-MAR-1999) to the EMBL/GenBank/DDBJ databases.
RL   MIPS, Am Klopferspitz 18a D-82152 Martinsried, GERMANY
XX
CC   Clone from S. Wiemann, sequenced by Qiagen within the cDNA
CC   sequencing consortium of the German Genome Project
CC   No s1 sequence available
CC   This clone is available at the RZPD in Berlin
CC   Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
CC   Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de
XX
FH   Key             Location/Qualifiers
FH
FT   source          1. .44
FT                   /db_xref="taxon:9606"
FT                   /organism="Homo sapiens"
FT                   /clone="DKFZp564K0763"
FT                   /clone_lib="564 (synonym: hfbr2). Vector pAMP1; host
FT                   Xl-2blue; sites NotI + SalI"
FT                   /dev_stage="fetal"
FT                   /tissue_type="brain"
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SQ   Sequence 44 BP; 21 A; 6 C; 10 G; 4 T; 3 other;

  Query Match             0.7%;  Score 20.8;  DB 2;  Length 44;
  Best Local Similarity   65.1%;  Pred. No. 1.8e+06;
  Matches   28;  Conservative    0;  Mismatches   15;  Indels    0;  Gaps    0;

Qy    2772 GGCGGGCCGCAGGGCCAGCCTGTTTCTCTAACAAACAAACAAA 2814
           || |||    || || || |  | |||| || ||| ||| |||
Db       2 GGGGGGNNANAGAGCAAGACCCTGTCTCAAAAAAAAAAAAAAA 44


RESULT 15
AZ602556/c
LOCUS       AZ602556                 45 bp    DNA     linear   GSS 13-DEC-2000
DEFINITION  1M0421E20F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
            clone UUGC1M0421E20 F, DNA sequence.
ACCESSION   AZ602556
VERSION     AZ602556.1  GI:11724746
KEYWORDS    GSS.
SOURCE      house mouse.
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 45)
  AUTHORS   Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
            Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly
            ,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.
            and Wright,D.,Weiss,R.
  TITLE     Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Robert B. Weiss
            University of Utah Genome Center
            University of Utah
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
            84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177
            Email: ddunn@genetics.utah.edu
            Insert Length: 10000   Std Error: 0.00
            Plate: 0421  row: E  column: 20
            Seq primer: CGTTGTAAAACGACGGCCAGT
            Class: plasmid ends
            High quality sequence stop: 45.
FEATURES             Location/Qualifiers
     source          1. .45
                     /organism="Mus musculus"
                     /strain="C57BL/6J"
                     /db_xref="taxon:10090"
                     /clone="UUGC1M0421E20"
                     /clone_lib="Mouse 10kb plasmid UUGC1M library"
                     /sex="Male"
                     /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
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/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

BASE COUNT 1 a 4 c 8 g 32 t
ORIGIN

Query Match 0.7%; Score 20.8; DB 17; Length 45;
Best Local Similarity 91.7%; Pred. No. 1.9e+06;
Matches 22; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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Qy   2799 CTAACAAACAAACAAACAAACAGC 2822
          |.|||||||||||||||||| |
Db     39 CAAACAAACAAACAAACAAACAAC 16
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Search completed: May 16, 2003, 10:26:05
Job time : 4055 secs